

GenCore version 5.1.3  
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CM nucleic acid - protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 01:16:09; Search time 46.5 Seconds  
(without alignments)

2768.174 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 941

Sequence: 1 gtagtgrtggtcccccaatg gctaccaccagattgagaar 483

Scoring table:

BLASTN62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DR seq length: 0

Maximum DR seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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LAOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi  
-LIST=45 -DORALIGN=200 -THP SCORE=PCP -THP MAX=100 -THP MIN=0 -ALIGN=15  
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-USER-US09882735 -ACCN 1 1 0 -strutab 03012003\_073942\_15203 -N-PU=6 -LCPU=3  
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Y-ACPOP=10 -YGAPEXT=0.5 -DELPE=6 -DELEXT=7

Database: A Geneseq 101002.\*

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23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	941	100.0	161	13	AA027496	Human soluble TNF
2	941	100.0	161	19	AAW59664	Human soluble TNF
3	941	100.0	161	19	AAW52767	Human soluble TNF
4	941	100.0	161	20	AAW89233	Human soluble TNF
5	941	100.0	161	22	AAW37676	Human soluble TNF
6	941	100.0	211	20	AAW89225	Human soluble TNF
7	941	100.0	280	22	AAW66979	Human soluble TNF
8	941	100.0	309	16	AAW70108	Human soluble TNF
9	941	100.0	311	20	AAW89229	Human soluble TNF
10	941	100.0	336	18	AAW33360	Human soluble TNF
11	941	100.0	366	20	AAW89228	Human soluble TNF
12	941	100.0	371	11	AAW07449	Human soluble TNF
13	941	100.0	397	20	AAW89227	Human soluble TNF
14	941	100.0	417	20	AAW89226	Human soluble TNF
15	941	100.0	420	20	AAW89224	Human soluble TNF
16	941	100.0	451	16	AAW70107	Human soluble TNF
17	941	100.0	455	12	AAW10986	Human soluble TNF
18	941	100.0	455	12	AAW11082	Human soluble TNF
19	941	100.0	455	13	AAW20787	Human soluble TNF
20	941	100.0	455	13	AAW24000	Human soluble TNF
21	941	100.0	455	14	AAW42059	Human soluble TNF
22	941	100.0	455	16	AAW75084	Human soluble TNF
23	941	100.0	455	20	AAW10934	Human soluble TNF
24	941	100.0	455	21	AAW36266	Human soluble TNF
25	941	100.0	455	21	AAW37800	Human soluble TNF
26	941	100.0	455	21	AAW26984	Human soluble TNF
27	941	100.0	455	21	AAW23446	Human soluble TNF
28	941	100.0	455	21	AAW01336	Human soluble TNF
29	941	100.0	455	22	AAW66817	Human soluble TNF
30	941	100.0	455	22	AAW36697	Human soluble TNF
31	941	100.0	455	22	AAW37677	Human soluble TNF
32	941	100.0	455	23	AAW81649	Human soluble TNF
33	941	100.0	455	23	AAW75764	Human soluble TNF
34	941	100.0	547	16	AAW70104	Human soluble TNF
35	941	100.0	884	16	AAW70103	Human soluble TNF
36	941	100.0	900	16	AAW70103	Human soluble TNF
37	941	100.0	1245	16	AAW70106	Human soluble TNF
38	941	100.0	1604	16	AAW70105	Human soluble TNF
39	938	99.7	455	11	AAW07451	Human soluble TNF
40	932	99.0	433	14	AAW51032	Human soluble TNF
41	932	99.0	443	14	AAW51033	Human soluble TNF
42	932	99.0	455	14	AAW42197	Human soluble TNF
43	932	99.0	455	14	AAW51034	Human soluble TNF
44	931	98.9	455	12	AAW12550	Human soluble TNF
45	930	98.9	909	19	AAW64485	Human soluble TNF

# ALIGNMENTS

## RESULT 1

AAW27496  
ID AAW27496 standard; protein, 161 AA.

XX AC AAW27496;

XX AC AAW27496;

DT 09-MAR-1993 (first entry)

XX AC AAW27496;

DE Native 30 kD TNF inhibitor.

XX AC AAW27496;

KW Tumour necrosis factor; ethylene glycol; pharmacokinetic;

KW adult respiratory distress syndrome; rheumatoid arthritis;

KW septic shock; pulmonary fibrosis; spacer.

XX AC AAW27496;

OS Homo sapiens.

XX AC AAW27496;

PN W00216221-A.

XX AC AAW27496;

PD 01-OCT-1992.

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XX 13-MAR-1992; 92WC-US02122.
XX
XX 15-MAR-1991; 91US-0669862.
XX
XX 17-JAN-1992; 92US-0844296.
XX
XX (SYND ) SYNERGEN INC.
XX
XX Arnes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;
XX
XX WPI, 1992-348933/42.
XX
XX New ethylene glycolated polypeptide(s) with improved
XX pharmacokinetic properties for treating e.g. TNF and IL-1
XX mediated diseases, e.g. adult respiratory distress syndrome,
XX rheumatoid arthritis, septic shock etc.
XX
XX Claim 54; Fig 2; 100pp; English.
XX
XX The sequence shows a native 30 kD TNF inhibitor which may be
XX modified to contain at least one non-native cysteine residue, pref.
XX at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is
XX joined to a non-peptidic polymer, pref. monomethoxy PEG via
XX thio-ether bonds. Two such TNF inhibitor moles. may be linked via
XX this non-peptidic spacer. The modified polypeptides show improved
XX pharmacokinetic properties, i.e. increased mol. wt. hence reduced
XX clearance rate following s.c. or systemic administration, increased
XX sol. of native TNF inhibitors, and reduced antigenicity. The
XX polypeptides may be used for treatment of TNF mediated diseases such
XX as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid
XX arthritis, inflammatory bowel disease and septic shock. The same
XX method may be applied to the interleukin-1 receptor antagonist
XX IL-1ra. See also AAR27495.
XX
XX Sequence 161 AA;
XX
XX Alignment Scores:
XX Pred. No.: 3,89e-86 Length: 161
XX Score: 941.00 Matches: 161
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 13 Gaps: 0
XX
XX US-09-882-735-1 (1-483) x AAR27496 (1-161)
XX
XX 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 60
XX 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20
XX
XX 41 AAGTTCACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX 21 LysCysHisLysLysLysTyrThrTyrLeuTyrAsnAspCysProGlnGlnAsnProThr 40
XX
XX 121 TGGAGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
XX 41 CysArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60
XX
XX 1st AGGTCCTCAAAATGCGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 240
XX 61 SerCysSerLysCysArgLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
XX
XX 441 CGGAGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
XX 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrIleHisTyrIleProSerGln 100
XX
XX 341 TTTCAAGTGTGTAATTCAGAGCTTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
XX 101 PheGlnCysPheAsnGlnCysSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 120
XX
XX 361 AAAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
XX 121 LysHisAsnThrValCysThrCysHisIleGlyPhePheLeuArgGlnAsnGlnCysVal 140

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XX 421 TCGTGTAGTACTGTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
XX 141 SerCysSerAsnGlnCysLysSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 160
XX
XX 481 AAT 483
XX
XX 161 Asn 161
XX
XX RESULT 2
XX ID AAW59664 standard; Protein; 161 AA.
XX
XX AAW59664;
XX
XX 28-SEP-1998 (first entry)
XX
XX Human soluble tumour necrosis factor receptor type I.
XX
XX Human; tumour necrosis factor; TNF; TNF receptor type I;
XX inflammatory disease; leukaemia; TNF binding protein;
XX anti-inflammatory drug; methotrexates.
XX
XX Homo sapiens.
XX
XX WC9824463-A2.
XX
XX 11-JUN-1998.
XX
XX 08-DEC-1997; 97WC-US22733.
XX
XX 09-JUL-1997; 97US-0052023.
XX
XX 06-DEC-1996; 96US-0032587.
XX
XX 23-JAN-1997; 97US-0036355.
XX
XX 07-FEB-1997; 97US-0039315.
XX
XX (AMGE-) AMGEN INC.
XX
XX Bendele AM, Edwards CK, Sennello RM;
XX
XX WPI; 1998-333039/29.
XX
XX N-PSDB; AAV41548.
XX
XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia -
XX by administering tumour necrosis factor binding protein and at least
XX one additional anti-inflammatory drug, e.g. methotrexate
XX
XX Disclosure; Fig 1; 104pp; English.
XX
XX This is the amino acid sequence of the human tumour necrosis factor
XX receptor type I, used in the method of the invention involving the
XX treatment of acute or chronic inflammatory disease such as leukaemia
XX by administering tumour necrosis factor binding protein and at least
XX one additional anti-inflammatory drug, e.g. methotrexate.
XX
XX Sequence 161 AA;
XX
XX Alignment Scores:
XX Pred. No.: 3,89e-86 Length: 161
XX Score: 941.00 Matches: 161
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 19 Gaps: 0
XX
XX US-09-882-735-1 (1-483) x AAW59664 (1-161)
XX
XX 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 60
XX 1 AspSerValCysProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 20
XX
XX 61 AAGTTCACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

```

Db 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 QY 121 TCACGAGTATTCACAGGAGTCTCTTACCGCTTCAGAAAACCCACCTCAGACACTGCCTC 180  
 Db 41 (YsArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 QY 181 AGTATATCTAAATATTAAGGAAATGAGTGGAGATCTCTTCTGCACAGTGGAC 240  
 Db 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 QY 241 CGGAGACACCTCTCTGCTGCTGAGGAGAACACGACCTACCGGATTTATGGAGTGAACCTT 300  
 Db 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisIstYrTrpSerGluAsnLeu 100  
 QY 301 TTCCACTGTTCAATTGGAGGCTTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 360  
 Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 QY 361 AAACACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 QY 421 TCCCTAGTAACTGTAAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
 Db 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 QY 481 AAT 483  
 Db 161 Asn 161  
 RESULT 3  
 AAW52267  
 ID AAW52267 standard; Protein; 161 AA.  
 AC AAW52267;  
 XX  
 DT 29-JUN-1998 (first entry)  
 XX  
 DE Soluble tumour necrosis factor receptor.  
 KW Soluble tumour necrosis factor receptor; TNFR: TNF-mediated disease;  
 KW tumour necrosis factor binding protein; autoimmune disease; arthritis;  
 KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;  
 KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.  
 XX  
 OS Homo sapiens.  
 PN W09801555-A2  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 09-JUL-1997; 97WO-US12244  
 XX  
 PR 04-MAR-1997; 97US-0039792  
 PR 09-JUL-1996; 96US-0021443  
 PR 06-DEC-1996; 96US-0032534  
 PR 23-JAN-1997; 97US-0037737  
 PR 07-FEB-1997; 97US-0039114  
 XX  
 PA (AMGE ) AMGEN INC.  
 XX  
 PI Edwards CK, Fisher EF, Kieft GL;  
 XX  
 DR WPI; 1998-101052/09.  
 DR N PSDB; AAV19801.  
 XX  
 PT Truncated and soluble forms of tumour necrosis factor receptor -  
 PT useful for treating diseases involving factor, e.g. arthritis and  
 PT adult respiratory distress syndrome  
 XX  
 PS Claim 1; Fig 1; 205pp; English.  
 XX  
 CC This sequence is the human soluble tumour necrosis factor receptor

CC (stnfr). The protein was used to make the truncated stnfr proteins of the  
 CC invention. The truncated stnfr proteins and tumour necrosis factor  
 CC binding proteins (TNBP) are used to treat any TNF-mediated disease,  
 CC e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia,  
 CC cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease  
 CC and other autoimmune diseases. Cells transformed with a vector containing  
 CC DNA encoding the protein may be used for production of recombinant stnfr,  
 CC which may also be used for measuring the amount of stnfr in samples and  
 CC to raise antibodies against stnfr. TNBP may also be used in preparation  
 CC of therapeutic compositions for treating the above diseases. The stnfr  
 CC proteins are well suited to large scale production (since they lack the  
 CC deamidation site in region 111-126, so are more stable in vivo) contain  
 CC fewer disulphide bonds and fewer epitopes, making them less antigenic  
 CC than full-length proteins.

SQ Sequence 161 AA;

#### Alignment Scores:

Pred. No.: 3,89e-86 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-882-735-1 (1-483) x AAW52267 (1-161)

QY 1 GATAGTGTGTCTCCCAAGGAAATAATATATCAACCTTAAATAATTTGTTCTTAC 40  
 Db 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysThr 20  
 QY 61 AAGTGCACACAAAGAACTATTTATTAATGACTGTCTAGAGGAGGAGGAGAAATATATAT 120  
 Db 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 QY 121 TGCAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 Db 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 QY 181 AGTGTCTCCAAATGCGAAAGAAATGCTTCAAGTGTGAGATCTCTTCTTCTGACACATGAG 240  
 Db 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 QY 241 CGGAGACACCGT 300  
 Db 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisIstYrTrpSerGluAsnLeu 100  
 QY 301 TTCAGTGTCTTCAATTGCAGGCTCTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 QY 361 AAACAGAACACCGT 420  
 Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 QY 421 TCCCTAGTAACTGTAAAGAAAGCTTATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
 Db 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 QY 481 AAT 483  
 Db 161 Asn 161  
 RESULT 4  
 AAW89233  
 ID AAW89233 standard; Protein; 161 AA.  
 XX  
 AC AAW89233;  
 XX  
 DT 04-MAR-1999 (first entry)  
 XX  
 DE Tumour necrosis inhibitor 30 kDa protein.

KM	Tumour necrosis factor receptor-1, TNFR-1, inhibitor, osteoprotegerin,
KW	OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KX	Inflammatory; apoptosis.
XX	
OS	Homo sapiens.
PN	WO9849305-A1.
ED	05-NOV-1998.
XX	
PF	23-APR-1998; 98MO-US06831.
XX	
PR	01-MAY-1997; 97US-0850188.
PA	(AMGEN) AMGEN INC.
XX	
EI	Baylor Inc., Wcoden S;
DR	WIPI; 1999-034661/03.
DP	N-PSSR: AAV81732.
XX	
PT	New chimeric osteoprotegerin polypeptides contain the
PT	osteoprotegerin dimerisation domain and a heterologous sequence,
PT	useful to treat TNF and TNFR-mediated disorders
XX	
PS	Disclosure, Fig 2, 2cfp, English.
CC	The present invention describes a chimeric polypeptide (A1), comprising
CC	an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC	amino acid sequence. Also described are: (1) a multimer polypeptide
CC	comprising covalently associated A1 monomers; (2) an isolated nucleic
CC	acid encoding A1; (3) an expression vector comprising the nucleic acid
CC	sequence; and (4) a host cell transformed or transfected with the
CC	expression vector so that the nucleic acid is expressible. The products
CC	from the present invention are useful to treat a variety of disorders
CC	including those related to receptor binding. Compositions comprising
CC	tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC	are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC	autoimmune diseases and disorders related to excessive apoptosis. The
CC	chimeras are also useful for detecting molecules which interact with
CC	fused heterologous sequences to identify potential new receptors and
CC	ligands. The present sequence represents the TNF inhibitor 30 kDa
XX	protein.
XX	
SQ	Sequence 161 AA:
Alignment Scores:	
Pred. NO.:	3,89e-86 Length: 161
Score:	941.00 Matches: 161
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	20 Gaps: 0
SV	CG-CY-B9Z-735-1 (1-483) x AAW89233 (1-161)
UY	1 GAATGTCTTGTCCTCAAGAAAAATTATCCACAACTCAATAATTCGATTGGTGTACC 60
DB	1 AsperValCySpGlnnglyLysTrillehtSPGInhamBserllecScyStr 20
UY	61 AAGTGCACAAGAAAACCTACTTTGACATGACTGTCCAGGCCGCGAGAGTAACGAC 120
DB	21 LysCysHisLysgLythrTrleutyVanapCysProgiLyginhapThrAsp 40
UY	121 TGACGGAAGTGTANAAAGTGGCTTTCTTCAATGCTTAGAAAAACCTCAACACCTGCTTC 180
DB	41 CysArgLysCysGlnSerGlySerPheThrAlaSerGIuaenhSlleuAghSLscylau 60
UY	181 AGTGTCTTCCAAAGCCGGAAGAAMAAGGCTCAGCGAGATCTCTTTCACAGCGAC 240
DB	61 SerLysSerLysCysArgLysGLMetArgLysInvalGluLeuSerSerCysThrValAsp 80
UY	241 CGGACACAGCATGTGTATGACAGAAAGAACAGTACCGGATTATGTGAGTGAACCTT 300

Accession	Protein	Length	Score
Db	81 ArgAspThrIleValCysGlyCysArgIleAsnGlnIleYrtrhgrhStYrTrpSerGluAsnIleu	100	3.89e-86
Qy	301 TTCAGTGCTTCAATTGAGACCTCTGCTCAATGAGACCGTGACCTCTCTGCGAGAG	360	941.00
Db	101 PheGlnCysPheAsnCysSerIleuCysIleuAsnGlyThrValHisIleuSerCysGlnGlu	120	
Qy	361 AACAAGAACACCGTGTGACCTGCGCATGACGAGTTCCTTCTTCAAGAGAAACGAGTGTC	420	
Db	121 LysGlnAsnThrIleValCysThrCysHisIAspIlePhePheLeuArgIleAsnGluCysVal	140	
Qy	421 TCCCTAGTAACTGTAGAAAAGCCTGGAGTGACGAGATTGTGCTTACCCAGATTGAG	480	
Db	141 SerCysSerAsnCysIlyLysSerIleuGlnCysThrIlySerIleuCysIleuProGlnIleGlu	160	
Qy	481 AAT 483		
Db	161 Asn 161		
RESULT 5			
AAB37676			
ID	AAB37676	standard; protein; 161 AA.	
AC	AAB37676;		
DT	02-MAR 2001 (first entry)		
XX	Human 30 kDa TNF inhibitor.		
DE	TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;		
XX	IL-1; inflammatory disease; degenerative disease; human.		
XX	Homo sapiens.		
XX	US6143866-A.		
XX	07-NOV-2000.		
XX	19 JAN 1995; 95US-0375242.		
XX	19-JUL-1990; 90US-0555274.		
XX	09-JUL-1993; 93US-0090366.		
XX	18-JUL-1989; 89US-0381080.		
XX	11-DEC-1989; 89US-0450329.		
XX	07-FEB-1990; 90US-0479661.		
XX	(AMGE-) AMGEN INC.		
XX	Squires C, King MW, Hale KK, Brewer MT, Thompson RC;		
XX	Vanderlidge RW, Vannice J, Kohno T;		
XX	WE1; 2001-006443/01.		
XX	N-PSDB; AAC83945.		
XX	Novel 30 kDa tumor necrosis factor inhibitor analog comprising a		
XX	PT non-native cysteine residue cross-linked with polyethylene glycol,		
XX	PT useful for treating inflammatory and degenerative diseases mediated by		
XX	TNF		
XX	Claim 1; Fig 19; 82pp; English.		
XX	The present invention relates to Tumour Necrosis Factor (TNF) inhibitors		
XX	(see AAB37676 and AAB37685), which have TNF inhibitory activity. The		
XX	novel TNF inhibitors of the present invention are useful as therapeutic		
XX	agents for inhibiting the activity of TNF and interleukin (IL-1), and		
XX	for treating inflammatory and degenerative diseases mediated by TNF. The		
XX	30 kDa TNF inhibitor can inhibit TNF alpha.		
XX	Sequence 161 AA;		
Alignment Scores:			
Pred. No.:		3.89e-86	161
Score:		941.00	161



Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US 09 882-735-1 (1-483) x AAB37676 (1-161)

1	QY	1	CATACTGTGTGTCCTCCCAAGGAAATAATATCCACCTCCAAAATAATTCGATTTCCTGTACC	60
	pb	1	AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr	20
	QY	61	AAGTGCACAAACCACTACTTGTACATAGTACTGTCCAGGCCCGGGCAGGATACGGAC	120
	pb	21	LysCysHisIysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	40
	QY	121	TCCAGTAAATGTTGAAGATGCTCTTCAACGGCTTCAGAAAAACACCTCAGACACTCCCTC	180
	pb	41	CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	60
	QY	181	AGCTGTCTCCAAATGCGAAAGAAATGGGTCAAGTGGAGATCTCTTCTTCACAGTGGAC	240
	pb	61	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp	80
	QY	241	CGGACACCCCTGTCTGGCTCCAGGAGACAGTACCGGCATTATTGGAGCTGAAACCTT	300
	pb	81	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisIstyrThrSerGluAsnLeu	100
	QY	301	TTCAGTGCCTTCAATTGCAGCCTCTGCCTCAATGGACCGTGCACCTCTCTCCACGAGG	360
	pb	101	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	120
	QY	361	AAACAGAACACCGTGTGCACCTGCTATGCAAGTCTTCTTCTTAAGAGAAAAACGAGTGTCT	420
	pb	121	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal	140
	QY	421	TCCTGTACTAACTCTAAGAAAGACCTGGAGTGCACGAGTTGTGCTTACCCAGATTGAG	480
	pb	141	SerCysSerAsnCysIysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	160
	QY	481	Asp 483	
	pb	161	Asn 161	
	RESULT	6		
	AAW89225			
110	AAW89225	standard, Protein, 211 AA.		

XXXX

AAWR9225;	
04 MAR-1999	(first entry)
	Tumour necrosis factor bp/osteoprotegerin construct TNFbp 4.0.
	Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
	CPG; chimeric; fusion; dimerisation domain; autoimmune disease;
	inflammation; apoptosis.
	Homo. sapiens.
	Synthetic.
	WO9849305 Al.
	05-NOV-1998.
	29-APR-1998; 98WO-US08631.
	01-MAY-1997; 97US-0850188.
	(AMGE-) AMGEN INC.
	Boyle WJ, Wooden S;
	WPI: 1999-014661/03

XX RESULT 7  
 XX ID AAB66979 standard; Protein: 280 AA.  
 XX AAB66979;  
 XX DT 19-APR-2001 (first entry)  
 XX DE Trilip protein.  
 XX  
 KM Date 1989, osteopetregerin, OPG, rheumatoid arthritis, hyperalgesia,  
 FM multiple sclerosis, osteoporosis, osteomyelitis, asthma, inflammation,  
 FM acute lupus erythematosus, graft versus host disease, septic shock,  
 FM acute pancreatitis, Alzheimer's disease, anorexia, altherosclerosis, pain,  
 FM endometrial cancer, myocardial infarction, cancer, diabetes, peptostasis,  
 KM endothelial cells, fever, osteoarthritis, inflammatory bowel disease,  
 KM ischaemia, Parkinson's disease.  
 XX  
 GS Unidentified.  
 XX  
 PN WO200103719-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 07-JUL-2006; 2006WD-US18667.  
 XX  
 PR 09-JUN-1999; 99US-0150670.  
 XX 09-FEB-1999; 99US-0457647.  
 XX  
 PA (AMOEBA) AMGEN INC.  
 XX  
 PI Boyle WJ, Lacey CL, Calzone FJ, Chang M, Senaldi G,  
 DR WP1: 2001 103031/11.  
 XX  
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
 PT multiple sclerosis and asthma, comprises administering an  
 PT osteopetregerin protein in conjunction with e.g. inhibitors of  
 PT interleukin and tumor necrosis factor alpha .  
 XX  
 PS Disclosure: Fig 2; 3lepp; English.

CC The present invention relates to a method for treating conditions leading  
 CC to bone loss. The method comprises administering a purified and isolated  
 CC osteopetregerin (OPG) protein (AA#F7836-AA#F7838 and AAB66974-AAB66976)  
 CC in combination with other substances such as tumour necrosis factor-alpha  
 CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
 CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet  
 CC activating factor (PAF) antagonists. The method is useful for treating  
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
 CC graft-versus-host disease (GVHD). Other diseases that can be treated  
 CC include acute pancreatitis, Alzheimer's disease, anorexia,  
 CC acute pancreatitis, primary biliary cirrhosis, J myocardial infarction,  
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
 CC psoriasis and septic shock. The present sequence was used in a sequence  
 CC homology comparison.  
 XX  
 SQ Sequence 280 AA:

Alignment Scores:			
Pred. No.:	Length:	Matches:	Score:
941.00	280	161	
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09 882-735-1 (1-483) X AAB66979 (1-280)  
 1 CAGACAGCCTGTCCCAAGAGAAATATATATCATTTTAAAATAATATCATTCATTGGCTGC 60

Db	41	AspSerValCysproIndmolYserTyrIleHisproIndmAsnSerIleCysYsThr	60
QY	61	AAAGGCCACAAAGAAACCTTACTTTGACATATCTGTCCAGGCTCCGAGATACGAGC	120
Db	61	LysCysHisLysGlyThrTyrIleuTyrAsnAspCysProGlyProGlyOlnAspThrAsp	80
QY	121	TGCAGGAGGTATAGAGAGGCTCTCTTCAACGCTTCAAAAACCACTTCAACATGGCTC	180
De	61	CysArgGlnCysLysSerGlySerPheThrAlaSerOlnAsnHisLeuArgHisCysLeu	100
QY	181	AGTTGTTCCAAATGTTGAAAAGAAATGAGTCAAGTCAAGTCTTTCTTGTGACATGAGC	240
De	101	SetCysSerCysCysLysAlaGlySerLysLeuGlyOlnValGlnIleGlySerCysThrValAsp	120
QY	241	CGGACACACCGTGTGTGTGTGTGACAGAAACACATACACGATATTATGTAGATAAAACTT	300
De	121	ArgAspThrValCysGlnCysArgLysAsnOlnTyrArgHisTyrTrpSerOlnAsnLeu	140
QY	301	TTCCAGTGGCTTCATATGCAAGCTCTGCTGATGTGAGAGAGAGAGAGAGAGAGAG	360
De	141	PheGlnCysPheAsnGlySerIleuGlySerLeuAsnGlyThrValHisLeuSerCysIndGln	160
QY	361	AAACAGAACACCGTGTGCACCTCCGATGCGAGTTCTTCTTTAAGAGAAAACAGAGTGTGC	420
De	161	LysHisAsnThrValCysThrCysHisAlaGlyPhePheLeuArgLysAsnGlnCysVal	180
QY	421	TCTCAGTAGTACATGTAGAGAAAGAGTGTAGTGTAGTGTAGTGTGTGTGTGTGTGTGTGT	480
De	181	SetCysSerAsnGlySerLysSerLeuGlnGlnCysHisLysLeuGlySerLeuArgProGlnIleGln	200
QY	481	AAT 483	
Db	201	Asn 201	
RESULT 8			
ID	AA70108	standard; Protein; 309 AA.	
AC	AA70108;		
XX	10-NOV-1995	(first entry)	
DT			
XX			
DE		TNF-R-GBH fusion protein.	
XX			
XX		Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein	
XX		res blood cell; cytokine receptor; glycoprotein binding peptide 130;	
XX		GMP 130; GBH; glycoprotein binding peptide homologue; glycoprotein A;	
XX		tumour necrosis factor receptor; TNF-R.	
OS		Chimeric Homo sapiens.	
OS		Chimeric Plasmodium falciparum.	
XX			
XX	Key	Location/Qualifiers	
XX	Misc-Difference	230..269	
FT		/label= repeat region	
FT		/note= "can be repeated n times, where n is a real	
FT		number"	
XX			
XX	MO9506737-A.		
XX			
XX	09-MAR-1995.		
XX			
XX	01-SEP-1994;	94WO-GB01900.	
XX			
XX	03-SEP-1993.	93GB-0018350.	
XX	23-AUG-1994.	94GB-0017021.	
XX			
XX	(PREN/) PRENDERGAST K F.		
XX			
XX	Prendergast KF;		
XX			
XX	WPI; 1995-115452/15.		

XX New hybrid peptide(s) for binding cytokine(s) - comprising a  
PT malaria parasite peptide capable of binding a red blood cell and  
PT a receptor peptide.  
XX  
XX Example A: Page 54-55; 93pp; English.  
XX  
XX Hybrid peptides for binding cytokines, comprising a malaria parasite  
CC (plasmodium falciparum) peptide (capable of binding to a red blood  
CC cell (RBC)) and a receptor peptide are claimed. AAR70103-25 are examples  
CC of these hybrid peptides. AAR70108 is a fusion of tumour necrosis factor  
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
CC and glycoprotein binding protein (GBP) homologue (GBP). The  
CC use of cytokine receptors not normally found on RBCs means that the  
CC cytokine can bind harmlessly to the RBC without deleterious effect.  
CC The RBC protects the hybrid peptides from excretion from the kidney, and  
CC due to steric hindrance prevents the cytokines binding to a receptor in  
CC another cell. GBP 130 or GBP are the pref. malaria parasite peptides  
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
CC PMMSA (pre major merozoite surface antigen) and the Duffy binding  
CC receptor molecule (eg. exhibited by plasmodium vivax). These peptides  
CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on the  
CC surface of RBCs. The hybrid peptides are thus used to lower the levels of  
CC free cytokines in the circulation to reduce pathological damage.

XX Sequence 309 AA;

Alignment Scores:  
Pred. No.: 4,66e-86 Length: 309  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-882-735-1 (1-483) x AAR70108 (1-309)

QY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTTCAAAATAATTCGATTTGCTGATCC 60  
Db 20 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 39  
QY 61 AATCTGTCACAAAGAACCTTGTGTAATGACTGTCTCCAGGCGCCGGCAGGATACCGAC 120  
Db 40 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 59  
QY 121 TGCAGGAGGTGTGAGAGCGCTCTCTTACCGCTTCAGAAACACCTCAGACACTGCCTC 180  
Db 60 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 79  
QY 181 AGCTGCTCCAAATGCCGAAGAAATGGGTGAGGTGGAGATCTCTTCTTGACACTGGAC 240  
Db 80 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 99  
QY 241 CGTCTACACCGTGTGCTGTCAGGAAGAACAGTACCGCATTTATGGAGTCAAAACCTT 300  
Db 100 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 119  
QY 301 TTCAGTGTCTCAATTCGACGCTCTCCCTCAATGGACCCGTGCACCTCTCTCTGCCAGGAG 360  
Db 120 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 139  
QY 361 AAACACAAACCTGTCTGACCTGCGATGAGGTCTTCTTAAGAGAAACGAGGTGCTC 420  
Db 140 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 159  
QY 421 TCCTCTTAGTAACTGTAAGAAAGCTGGAGTGCACGAAGCTTGTGCTACCCAGATTGAG 480  
Db 160 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 179  
QY 481 AAT 483  
Db 180 Asn 180

RESULT 9  
AAW89229  
ID AAW89229 standard; Protein, 311 AA.  
AC AAW89229;  
XX  
XX 04-MAR-1999 (first entry)  
XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/104.  
XX  
XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
XX OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
XX Inflammation; apoptosis.  
XX Homo sapiens.  
XX Synthetic.  
XX WO9849305-A1.  
XX 05-NOV-1998.  
XX 29-APR-1998; 98WO-US08631.  
XX 01-MAY-1997; 97US-0850188.  
XX (AMGE-) AMGEN INC.  
XX Boyle WJ, Wooden S;  
XX WPI; 1999-034661/03.  
XX  
XX New chimeric osteoprotegerin polypeptides - contain the  
XX osteoprotegerin dimerisation domain and a heterologous sequence,  
XX useful to treat TNF and TNFR-mediated disorders  
XX  
XX Example 1; Fig 4; 92pp; English.  
XX

CC The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.

XX Sequence 311 AA;

Alignment Scores:

Pred. No.: 4,67e-86 Length: 311  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 20 Gaps: 0

US-09-882-735-1 (1-483) x AAW89229 (1-311)

QY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTTCAAAATAATTCGATTTGCTGATCC 60  
Db 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60  
QY 61 AAGTGCACAAAGGACCTACTGTGACATCACTCTCCAGTCCGAGTCCGAGTATACAC 120  
Db 120







KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.

OS Homo sapiens.

OS Synthetic.

PN WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (Al), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated Al monomers; (2) an isolated nucleic  
 CC acid encoding Al; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.

XX Sequence 417 AA;

XX Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
5,06e-86	941.00	417	161
Percent Similarity:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
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US 09 882-735-1 (1 493) X AAW89226 (1 417)

QY 1 GATATGTTGTCCTCCAGGAAATATATCCACCTTCAAAATAATTCGATTGCTGACC 60  
 DB 41 AspSerValCysProGlnGlyIleHisProGlnAsnSerIleCysCysThr 60  
 QY 61 AAGTCGCACAAATGAACTTCTTACATCTCTCCAGTCCAGTCCGCGGAGATACGGAC 120  
 DB 61 LysCysHisLysGlyThrIleLeuIleAsnAspCysProGlyProGlyGlnAspThr 80  
 QY 121 TGCACAGTCTGTATAGTGTCTCTCTCCACCTTCCAGGAAATCCACCTCAGACATGCTC 180  
 DB 81 CysArgGluCysCysLeuSerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
 QY 181 AGCTGCTCCAAATGCGGAAAGGAAATGAGTCTGAGGTGAGATCTTCTTTCACAGTGGAC 240  
 DB 101 SerCysSerLysCysArgGlyGluMetGlyGlnValGluIleSerSerCysThrValAsp 120  
 QY 241 CGGATACAGCTGTCTCTGCTGGCAGGAAACAGTACCGGACATTATTGAGCTGAAACCTT 300

DB 121 ArgAspThrValCysGlyCysArgLysAsnGluTyrArgHisTyrTrpSerGluAsnLeu 140  
 QY 301 TTCCAGTCTTCAATTGACGCTGCTCAATGAGAGCTGACCTCTCTCTCAATGAG 460  
 DB 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnHis 160  
 QY 361 AACAGAACACCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180  
 QY 421 TCCTGTAGTAACTGTAAAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
 DB 181 SerCysSerAsnCysLysSerLeuGluCysThrIleLeuCysLeuProGlnIleGlu 500  
 QY 481 AAT 483  
 DB 201 Asn 201  
 RESULT 15  
 AAW89224  
 ID AAW89224 standard; Protein; 420 AA.  
 XX  
 AC AAW89224;  
 XX  
 DT 04-MAR-1999 (first entry)  
 XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.  
 DE  
 XX Tumour necrosis factor receptor 1, TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO9849305-A1.  
 XX 05-NOV-1998.  
 XX 29-APR-1998; 98WO-US08631.  
 XX 01-MAY-1997; 97US-0850188.  
 XX (AMGE-) AMGEN INC.  
 XX Boyle WJ, Wooden S;  
 XX WPI; 1999-034661/03.  
 XX New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (Al), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated Al monomers; (2) an isolated nucleic  
 CC acid encoding Al; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.





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CM nucleic protein search, using frame\_plus\_n2p model  
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(without alignments)  
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Perfect score: 941  
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Scoring table: BLOSUM62  
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

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Post processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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2	941	100.0	280	3	US-08-974-022-46
3	941	100.0	280	4	US-08-795-445A-46
4	941	100.0	280	4	US-08-795-447A-46
5	941	100.0	280	4	US-08-974-186-46
6	941	100.0	280	4	US-08-795-446B-46
7	941	100.0	280	4	US-08-704-945D-13
8	941	100.0	336	4	US-08-804-166-8
9	941	100.0	336	4	US-08-910-991-8
10	941	100.0	455	1	US-08-050-319B-25
11	941	100.0	455	1	US-08-321-668-2
12	941	100.0	455	1	US-08-837-941-2

13	941	100.0	455	2	US-08-126-016-2	Sequence 2, Appl
14	941	100.0	455	2	US-08-465-982-25	Sequence 25, Appl
15	941	100.0	455	4	US-08-815-469-5	Sequence 5, Appl
16	941	100.0	455	4	US-09-006-353A-3	Sequence 3, Appl
17	941	100.0	455	4	US-09-527-236A-5	Sequence 5, Appl
18	941	100.0	455	4	US-08-054-970-2	Sequence 2, Appl
19	941	100.0	455	4	US-09-565-918-4	Sequence 4, Appl
20	941	100.0	455	4	US-09-573-986-3	Sequence 4, Appl
21	930.5	98.9	909	4	US-09-013-895A-4	Sequence 4, Appl
22	930.5	98.9	909	4	US-09-448-868-4	Sequence 4, Appl
23	928	98.6	285	4	US-08-804-166-6	Sequence 6, Appl
24	928	98.6	285	4	US-08-910-991-6	Sequence 6, Appl
25	925.5	98.4	453	4	US-09-086-483A-5	Sequence 5, Appl
26	924	98.2	199	1	US-08-050-319B-48	Sequence 48, Appl
27	924	98.2	199	2	US-08-465-982-48	Sequence 48, Appl
28	921	97.9	137	4	US-08-828-683A-21	Sequence 21, Appl
29	904	96.1	154	4	US-08-828-683A-12	Sequence 12, Appl
30	900	95.6	153	4	US-08-219-237B-4	Sequence 4, Appl
31	900	95.6	153	4	US-08-477-347-12	Sequence 12, Appl
32	900	95.6	153	4	US-08-476-862-3	Sequence 3, Appl
33	900	95.6	153	4	US-08-468-560C-4	Sequence 4, Appl
34	873	92.8	154	2	US-08-212-087A-10	Sequence 10, Appl
35	842.5	89.5	256	4	US-08-804-166-2	Sequence 2, Appl
36	842.5	89.5	256	4	US-08-910-991-2	Sequence 2, Appl
37	837	88.9	307	4	US-08-804-166-4	Sequence 4, Appl
38	837	88.9	307	4	US-08-910-991-4	Sequence 4, Appl
39	822	87.4	139	4	US-08-706-945C-129	Sequence 129, Appl
40	746	79.3	167	1	US-08-050-319B-2	Sequence 2, Appl
41	746	79.3	167	1	US-08-050-319B-57	Sequence 57, Appl
42	746	79.3	167	2	US-08-465-982-2	Sequence 2, Appl
43	746	79.3	167	2	US-08-465-982-57	Sequence 57, Appl
44	731	77.7	124	1	US-08-050-319B-4	Sequence 4, Appl
45	731	77.7	124	2	US-08-465-982-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-326-394-2  
; Sequence 2, Application US/09326394  
; Patent No. 6306820  
GENERAL INFORMATION:  
; APPLICANT: Bendele, Alison M.  
; APPLICANT: Sennello, Regina M.  
; APPLICANT: Edwards, Carl K.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/932,587  
; FILING DATE: 06-DEC-1996  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,345  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07-FEB-1997

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 66/052,023  
 FILING DATE: 09-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lindrick, Thomas K.  
 REGISTRATION NUMBER: 32,185  
 PREFERENCE/DOCKET NUMBER: A-430D  
 INFORMATION FOR SEQ ID NO. 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 161 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-326 394-2

Alignment Scores:  
 Pred. No.: 2,93e-87 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-882-735-1 (1-483) x US-09-326 394 2 (1-161)

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UY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTTCAAAATTAATTGATTGCTGTACC 60
Db 1 AspservAlcysProginglyllystYrllenhsproglnasnserilecysCysThr 20
UY 61 AAGTCCCAAGAAAGAACTTCTTACATGATGTCAGGCGCGGCGGCGGCGGCGGCGGCGG 120
Db 21 LysCysHslsYsglyThrTyrleuTyraasnpsrCysProglyProglyGlnAspThrAsp 40
UY 121 TGCAGGAGTGTGAGAGCGGCTTCCACCGCTTCAGAAACCACTGACACTGCTTC 180
Db 41 CysArgGlnCysGlnserGlySerPheThrAlaSerGlnAsnHslsleuArgHslsCysleu 60
UY 161 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 61 SerCysSerLysCysArgLysGlnmetGlyGlnValGlnIleSerSerCysThrValAsp 80
UY 241 CCGGACACCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 81 ArgAspThrValCysGlnCysArgLysAsnGlnIleTyraHslsTyrrpsrGlnAsnleu 100
UY 301 TTCAGTGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
Db 101 PheGlnCysPheAsnCysSerleuGlnCysleuAsnGlyThrValHslsSerCysGlnGln 120
UY 361 AAACAGAACACCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 121 LysGlnAsnThrValCysThrCysHslsAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140
UY 421 TCTGTAGTACTGTAAAGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 141 SerCysSerAsnCysLysLysSerleuGlnCysThrLysleuGlnCysleuProGlnIleGln 160
UY 481 AAT 483
Db 161 Asn 161

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RESULT 2

US-08-974-022-46  
 Sequence 46, Application US/08974022

Patent No. 661558  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calcione, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
 STREET: 1840 Denavilland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,022  
 FILING DATE: 12-DEC-1995

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/577,788  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 280 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-974-022-46

Alignment Scores:  
 Pred. No.: 3,38e-87 Length: 280  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-882-735-1 (1-483) x US-08-974-022-46 (1-280)

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UY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTTCAAAATTAATTGATTGCTGTACC 60
Db 41 AspservAlcysProginglyllystYrllenhsproglnasnserilecysCysThr 60
UY 61 AAGTCCCAAGAAAGAACTTCTTACATGATGTCAGGCGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 LysCysHslsYsglyThrTyrleuTyraasnpsrCysProglyProglyGlnAspThrAsp 80
UY 121 TGCAGGAGTGTGAGAGCGGCTTCCACCGCTTCAGAAACCACTGACACTGCTTC 180
Db 81 CysArgGlnCysGlnserGlySerPheThrAlaSerGlnAsnHslsleuArgHslsCysleu 100
UY 181 AGTGTCTCAATATGCCAAGAAATGAGTCAAGTGTGAGATGCTTCTTTCACAGTGGAC 240
Db 101 SerCysSerLysCysArgLysGlnmetGlyGlnValGlnIleSerSerCysThrValAsp 120
UY 241 CCGGACACCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 121 ArgAspThrValCysGlnCysArgLysAsnGlnIleTyraHslsTyrrpsrGlnAsnleu 140
UY 301 TTCAGTGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
Db 141 PheGlnCysPheAsnCysSerleuGlnCysleuAsnGlyThrValHslsSerCysGlnGln 160
UY 361 AAACAGAACACCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 161 LysGlnAsnThrValCysThrCysHslsAlaGlyPhePheLeuArgGlnAsnGlnCysVal 180
UY 421 TCTGTAGTACTGTAAAGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 181 SerCysSerAsnCysLysLysSerleuGlnCysThrLysleuGlnCysleuProGlnIleGln 200
UY 481 AAT 483

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Db 201 Asn 201
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RESULT 3
US-08-795-445A-46
; Sequence 46, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/795,445A
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO. 46:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-46

Alignment Scores:
Pred. No.: 3,38e-87 Length: 280
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 4
US-08-882-735-1 (1-483) x US-08-795-445A-46 (1-280)

QY 1 GATAGTGTGTGCCCCAGGAAATATATCCACCTCAAAATTAATTCGATTGCTGTACC 60
Db 41 AspSerValCysProGlnGlySerThrHisProGlnAsnAsnSerIleCysCysThr 60
QY 61 AAGTGTGACAAAGGAACTACTTGTACAAATGCTCCAGGCGCGGCGGAGATACGAC 120
Db 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 80
QY 121 TGCATGACCTGTGACAGGCGGCTTCCGCTTACGAAACACCTCCAGACATGCTC 180
Db 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
QY 181 AGTGTGTGCTGCCCCAGGAAATATATCCACCTCAAAATTAATTCGATTGCTGTACC 240
Db 101 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
QY 241 CGACACCTGTTGTATGTGTAAGAACTAGTACCTGCTATTATTCGAGTGAACCTT 300
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Db 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 148
QY 301 TTCCAGTGTTCGAATTCAGGCTCTGCTCAATGATGATGATGATGATGATGATGATG 160
Db 141 PheGlnCysPheAsnCysSerLeuGlyCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
QY 361 AAACAGAACACCGTGTGTCACCTGCGATGCGAGTTTCTTCTTAAAGAGAAAAGATTTGTC 420
Db 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
QY 421 TCCTGTACTAAGTGTAGAGAAAGGCTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 480
Db 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
QY 481 AAT 483
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Db 201 Asn 201

RESULT 4
US-08-795-447A-46
; Sequence 46, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/795,447A
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO. 46:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-447A-46

Alignment Scores:
Pred. No.: 3,38e-87 Length: 280
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 4
US-08-882-735-1 (1-483) x US-08-795-447A-46 (1-280)

QY 1 GATAGTGTGTGCCCCAGGAAATATATCCACCTCAAAATTAATTCGATTGCTGTACC 60
Db 41 AspSerValCysProGlnGlySerThrHisProGlnAsnAsnSerIleCysCysThr 60
QY 61 AAGTGTGACAAAGGAACTACTTGTACAAATGCTCCAGGCGCGGCGGAGATACGAC 120
Db 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 80
QY 121 TGCATGACCTGTGACAGGCGGCTTCCGCTTACGAAACACCTCCAGACATGCTC 180
Db 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
QY 181 AGTGTGTGCTGCCCCAGGAAATATATCCACCTCAAAATTAATTCGATTGCTGTACC 240
Db 101 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
QY 241 CGACACCTGTTGTATGTGTAAGAACTAGTACCTGCTATTATTCGAGTGAACCTT 300
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APPLICATION NUMBER: 08/577,788  
FILING DATE: 1995 12 22  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/POCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US 08 795-446B 46

Alignment Scores:  
Pred. No.: 3.38e-87 Length: 280  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US 09-882-735-1 (1-483) x US 08-795-446B-46 (1-280)

QY 1 GATAGTGTGTCTGTCGCAAGGAAATATATATACACCTCAAAATAATTGCTGTACC 60  
DB 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60  
QY 61 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCGGSEACATACGGAC 120  
DB 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80  
QY 121 TCCAGGAGCTGTACAGCGGTCTTCTTCACTGCTTACAGAAACCACTTACACACTGCTC 180  
DB 81 CysArgGlnCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
QY 181 AGCTGCTCAAAATGCGGAAGCAATGCGTCACTGAGAGCTCTTCTTCACTGCTTACAGAA 240  
DB 101 SerCysSerLysCysArgLysGlnMetGlyGlnValGluIleSerSerCysThrValAsp 120  
QY 241 CCGACACAGCTGTGTGCTGTGAGGAAGACAGTACCGGCAATTATGAGTGAAGAACTT 300  
DB 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 140  
QY 301 TTCCAGTGTCTCAATGGAGCTTGTGCTCAATGGAGCGCGTGCACCTCTCTCTGCCAGGAG 360  
DB 141 PheGlnCysPheAsnCysSerLeuAsnGlyThrValHisLeuSerCysGlnGlu 160  
QY 361 AAACAGACACCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180  
QY 421 TCTCTTACTTAATGTAAGAAAGCTGGAGTGCACGAAGTGTGCTTACCCAGATTGAG 480  
DB 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200  
QY 481 AAT 483  
DB 201 Asn 201

RESULT 7  
US 08-706-945D-132  
Sequence 132, Application US/08706945D  
Patent No. 6369027  
GENERAL INFORMATION:  
APPLICANT: Boyle, William  
APPLICANT: Lacey, David  
APPLICANT: Calzone, Frank  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
FILE REFERENCE: A-378CIP  
CURRENT APPLICATION NUMBER: US/08/706,945D  
CURRENT FILING DATE: 1996-09-03

PRIOR APPLICATION NUMBER: 08/577,788  
PRIOR FILING DATE: 1995 12 22  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 132  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-706-945D-132

Alignment Scores:  
Pred. No.: 3.38e-87 Length: 280  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US 09-882-735-1 (1-483) x US-08-706-945D-132 (1-280)

QY 1 GATAGTGTGTCTGTCGCAAGGAAATATATATACACCTCAAAATAATTGCTGTACC 60  
DB 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60  
QY 61 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCGGSEACATACGGAC 120  
DB 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80  
QY 121 TCCAGGAGCTGTACAGCGGTCTTCTTCACTGCTTACAGAAACCACTTACACACTGCTC 180  
DB 81 CysArgGlnCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
QY 181 AGCTGCTCAAAATGCGGAAGCAATGCGTCACTGAGAGCTCTTCTTCACTGCTTACAGAA 240  
DB 101 SerCysSerLysCysArgLysGlnMetGlyGlnValGluIleSerSerCysThrValAsp 120  
QY 241 CCGACACAGCTGTGTGCTGTGAGGAAGACAGTACCGGCAATTATGAGTGAAGAACTT 300  
DB 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 140  
QY 301 TTCCAGTGTCTCAATGGAGCTTGTGCTCAATGGAGCGCGTGCACCTCTCTCTGCCAGGAG 360  
DB 141 PheGlnCysPheAsnCysSerLeuAsnGlyThrValHisLeuSerCysGlnGlu 160  
QY 361 AAACAGACACCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180  
QY 421 TCTCTTACTTAATGTAAGAAAGCTGGAGTGCACGAAGTGTGCTTACCCAGATTGAG 480  
DB 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200  
QY 481 AAT 483  
DB 201 Asn 201

RESULT 8  
US-08-804-166-8  
Sequence 8, Application US/08804166  
Patent No. 6193972  
GENERAL INFORMATION:  
APPLICANT: Campbell, Robert K.  
APPLICANT: Jameson, Bradford A.  
APPLICANT: Chappel, Scott C.  
TITLE OF INVENTION: HYBRID PROTEINS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOURCE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brody, Robert L.
REGISTRATION NUMBER: 29,618
REFERENCE/DOCKET NUMBER: CAMPBELL, 2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-804-166-8

Alignment Scores:
Pred. No.: 3,548-87
Score: 941.00
Length: 336
Percent Similarity: 100.00%
Matches: 161
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Query Match: 100.00%
Indels: 0
Gaps: 0
DB: 4
(US-08-804-166-8 (1-483) X US-08-804-166-8 (1-336))

CY 1 GATATCTGTGTCTGCAAGGAAATATATCTTCACTTAAATTTGATTGCTGAC 60
DE 23 Asperteralysproindilyltyrilehtsprindnsnseritlcyssythr 42
CY 44 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 120
DE 43 Lyscyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 62
CY 124 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 180
DE 63 Cysargylgysproindilyltyrilehtsprindnsnseritlcyssythr 82
CY 181 AGTGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 240
DE 93 Sercyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 102
CY 241 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 300
DE 103 Argargprtnvalcysglycysargylgysasnolnlyrlyrlyrlyrlyrlyr 122
CY 361 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 360
DE 123 Proindilyltyrilehtsprindnsnseritlcyssythr 142
CY 361 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 420
DE 143 Lyscyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 162
CY 421 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 480
DE 163 Sercyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 182
CY 481 AAT 483
DE 183 Asn 183

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RESULT 9
US-08-910-991-8
Sequence 8, Application US/08910991
Patent No. 6194177
GENERAL INFORMATION:
APPLICANT: Campbell, Robert L.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street N W , Ste 300
CITY: Washington
STATE: D C
COUNTRY: USA
ZIP: 22307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL, 2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-991-8

Alignment Scores:
Pred. No.: 3,548-87
Score: 941.00
Length: 336
Percent Similarity: 100.00%
Matches: 161
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Query Match: 100.00%
Indels: 0
Gaps: 0
DB: 4
(US-08-882-735-1 (1-483) X US-08-910-991-8 (1-336))

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DE 23 Asperteralysproindilyltyrilehtsprindnsnseritlcyssythr 42
CY 44 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 120
DE 43 Lyscyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 62
CY 124 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 180
DE 103 Argargprtnvalcysglycysargylgysasnolnlyrlyrlyrlyrlyrlyr 122
CY 361 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 360
DE 123 Proindilyltyrilehtsprindnsnseritlcyssythr 142
CY 361 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 420
DE 143 Lyscyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 162
CY 421 AGAGTCTGCAAAATGCGAAATGAGTATCTTCACTTCACTTCACTTCACTTCA 480
DE 163 Sercyshtlsglythrlyrleantyrasnaspysproglyproglylnasprtmasp 182
CY 481 AAT 483
DE 183 Asn 183

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QY 301 TTCCAGTGTCTTAAATTAAGATGAGTGTGATTAATGAGACCGTGCACCTCTCTCCGCAAGAG 360
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QY 481 AAT 483
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Db 183 Asn 183

RESULT 10
US-08-050-319B-25
; Sequence 25, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10 May 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-25

Alignment Scores:
Prod. No.: 3-83e-87 Length: 455
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-882-735-1 (1-483) x US-08-050-319B-25 (1-455)
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QY 121 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCGAAAACGACCTCAGACATGTGTC 180
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QY 421 TCTGTATTAATTTAAGAGAAAGCTGAGTGCAGAGAGTGTGCTCAACCCAGATTGAG 480
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QY 481 AAT 483
|||
Db 201 Asn 201

RESULT 11
US-08-321-668-2
; Sequence 2, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARELOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEEDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528

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QY 481 AAT 483  
Db 201 Asn 201

## RESULT 13

US-08-126-016-2

; Sequence 2, Application US/08126016  
; Patent No. 5811261  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, DAVID  
; APPLICANT: KOPHAR, YARON  
; APPLICANT: KEMPER, OLIVER  
; APPLICANT: ENGELMANN, HARTMUT  
; APPLICANT: BRAKERUSCH, COPO  
; APPLICANT: ADERKA, DAN  
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
; NECTROSIS FACTOR BINDING PROTEIN I (TBP-I)  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/126.016  
; FILING DATE: 24-SEP-1993  
; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/625668  
; FILING DATE: 13-DEC-1990

; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, FOGEL L.  
; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-747-4524

; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US 08 126-016-2

## Alignment Scores:

Pred. No.:	Length:	Score:
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100.00%	Conservative:	0
100.00%	Mismatches:	0
100.00%	Indels:	0
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US-09 882-735-1 (1-483) x US-08 126 016 2 (1-455)

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Db 41 AspSerValCysProGlnGlyIleHisProGlnAsnSerIleCysCysThr 60  
QY 61 AACTGTCACAAAGGACCTACTTGTACATGCTCCAGCGCGGCGGACGAGTACCGAC 120  
Db 61 CysCysHisIleGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 80  
QY 121 TGTATGACTGTGAGATGGGTGTTTAAATTTCAAGAAACCACTCAGACATGCTC 180

Db 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
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Db 101 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 120  
QY 241 CCGACACAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400  
Db 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 140  
QY 301 TTCAGTGTCTTCAATTCAGACCTCTGCTTCAATGAGAGCTGCTGCTGCTGCTGCT 600  
Db 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160  
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QY 421 TCCTGTAGTAACTGTAAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 181 SerCysSerAsnCysLysLysSerLeuGluCysThrIleLysLeuCysLeuProGlnIleGlu 200  
QY 481 AAT 483  
Db 201 Asn 201

## RESULT 14

US-08-465-982-25

; Sequence 25, Application US/08465982  
; Patent No. 5863786

; GENERAL INFORMATION:

; APPLICANT: M. Feldmann, P. W. Gray,  
; APPLICANT: M. J. C. Turner, F. M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; NECTROSIS FACTOR alpha) Receptor

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Peed & Robbins  
; STREET: 635 Bryant Street

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, version #1.25

; CURRENT APPLICATION DATA: US/08/465,982

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/050,319

; FILING DATE: 10-May-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Robbins, Roberta L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5150-0030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 617-8999

; TELEFAX: (415) 327-3231

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 455 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-465-982-25

Alignment Scores:

Pred. No.:	Length:	Score:
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US-C9 882-135-1 (1 483) X US 08 465 982-25 (1 455)

25 11 455

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Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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Sup:

Sup:

Sup:

US-C9 882-135-1 (1 483) X US 08 465 982-25 (1 455)

GenCore version 5.1.3

Copyright (c) 1993 - 2003 CompuGen Ltd.

CM nucleic acid protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 03:44:00 / Search time 29.5 Seconds  
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620,582 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 941

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Listing first 45 summaries

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FGAPEXT=7 YGAPOP=10 YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	941	100.0	161	9	US-09-882-734-4 Sequence 4, Appl
3	941	100.0	161	9	US-09-882-734-4 Sequence 4, Appl
4	941	100.0	161	10	US-09-882-734-4 Sequence 4, Appl

5	941	100.0	161	10	US-09-882-734-4 Sequence 2, Appl
6	941	100.0	162	9	US-09-882-734-4 Sequence 6, Appl
7	941	100.0	162	10	US-09-882-734-4 Sequence 9, Appl
8	941	100.0	162	10	US-09-882-734-4 Sequence 20, Appl
9	941	100.0	172	9	US-09-882-734-4 Sequence 16, Appl
10	941	100.0	173	9	US-09-882-734-4 Sequence 10, Appl
11	941	100.0	183	9	US-09-882-734-4 Sequence 18, Appl
12	941	100.0	190	9	US-09-882-734-4 Sequence 12, Appl
13	941	100.0	200	9	US-09-882-734-4 Sequence 8, Appl
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40	933	99.1	162	9	US-09-882-734-4 Sequence 21, Appl
41	931	98.6	271	9	US-09-882-734-4 Sequence 22, Appl
42	928	98.6	285	10	US-09-882-734-4 Sequence 20, Appl
43	928	98.6	285	10	US-09-882-734-4 Sequence 6, Appl
44	927	98.5	162	10	US-09-882-734-4 Sequence 19, Appl
45	921	97.9	157	9	US-09-882-734-4 Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-09-882-734-4  
Sequence 4, Application US/09898234  
Patent No. US20020155112A1  
GENEPAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolf  
APPLICANT: Maurer-Poggy, Ingrid  
APPLICANT: Strataflow, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98,385-1  
CURRENT APPLICATION NUMBER: US/99/898,234  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161

TYPE: FRT  
ORGANISM: Homo sapiens  
US-09-898-234-4

## Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
941.00	100.00%	161	161	0	0	0	0
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Query Match:	100.00%						

US-09-882-735-1 (1-483) x US-09-898-234-4 (1-161)

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1  LysCysHisLysGlyThrTyrIleuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
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1  ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlnAsnLeu 100
1  TCCGTGTACTGTAAGTGAAGAAAGCCCTGAGTGCAGCAAGTTGCTCCAGGAGGAG 360
1  PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGln 120
1  AAGTCCCAAAAGGAACTTCTGTACAAATGACTGTCCAGGCCCGGAGGAGATACGAGAC 420
1  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140
1  TCCGTGTACTGTAAGTGAAGAAAGCCCTGAGTGCAGCAAGTTGCTCCAGGAGGAG 480
1  SerCysSerAsnCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGln 160
481 AAT 483
161 Asn 161

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RESULT 2  
US-09-899-429A-4  
Sequence 4, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899-429A  
CURRENT FILING DATE: 2001-07-03  
PRIORITY FILING DATE: 09/792,356  
PRIORITY FILING DATE: 2000-02-23  
PRIORITY FILING DATE: 1995-06-07  
PRIORITY FILING DATE: 08/477,639  
PRIORITY FILING DATE: 1995-02-01  
PRIORITY FILING DATE: 08/153,267  
PRIORITY FILING DATE: 1993-11-17  
PRIORITY APPLICATION NUMBER: 07/821,750

PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: FRT  
ORGANISM: Homo sapiens  
US-09-899-429A-4

## Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
941.00	100.00%	161	161	0	0	0	0
Best Local Similarity:	100.00%						
Query Match:	100.00%						

US-09-882-735-1 (1-483) x US-09-899-429A-4 (1-161)

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1  GATAGTGTGTGTCCTCCAGAGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 60
1  AsperterValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20
1  AAGTCCCAAAAGGAACTTCTGTACAAATGACTGTCCAGGCCCGGAGGAGATACGAGAC 120
1  LysCysHisLysGlyThrTyrIleuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
1  TGCAAGAGAGTGTGAGAGCGGCTCCCTCAGCCGCTTCAGAAAACCACTCAGACACTGCTTC 180
1  CysArgGlnCysGlnSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60
1  AAGTCCCAAAAGGAACTTCTGTACAAATGACTGTCCAGGCCCGGAGGAGATACGAGAC 240
1  SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
1  TGCAAGAGAGTGTGAGAGCGGCTCCCTCAGCCGCTTCAGAAAACCACTCAGACACTGCTTC 300
1  ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlnAsnLeu 100
1  TCCGTGTACTGTAAGTGAAGAAAGCCCTGAGTGCAGCAAGTTGCTCCAGGAGGAG 360
1  PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGln 120
1  AAGTCCCAAAAGGAACTTCTGTACAAATGACTGTCCAGGCCCGGAGGAGATACGAGAC 420
1  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140
1  TCCGTGTACTGTAAGTGAAGAAAGCCCTGAGTGCAGCAAGTTGCTCCAGGAGGAG 480
1  SerCysSerAsnCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGln 160
481 AAT 483
161 Asn 161

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RESULT 3  
US-09-792-356-4  
Sequence 4, Application US/09792356  
Publication No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-G  
CURRENT APPLICATION NUMBER: US/09/792,356  
CURRENT FILING DATE: 2001-08-17  
PRIORITY FILING DATE: 08/477,639  
PRIORITY APPLICATION NUMBER: 07/821,750

; PRIOR APPLICATION NUMBER: 08/383,676  
 ; PRIOR FILING DATE: 1995-02-01  
 ; PRIOR APPLICATION NUMBER: 09/153,287  
 ; PRIOR FILING DATE: 1993-11-17  
 ; PRIOR APPLICATION NUMBER: 07/821,750  
 ; PRIOR FILING DATE: 1992-01-02  
 ; PRIOR APPLICATION NUMBER: 07/511,430  
 ; PRIOR FILING DATE: 1990-04-20  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 161  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US 09 792-356-4

Alignment Scores:  
 Pred. No.: 4 38e-80 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US 09 882-735-1 (1-483) x US-09-792-356-4 (1-161)  
 QY 1 GATAGTGTGTGTCCTCCCAAGAAATATATACACCTCAAAATAATTCGATTGTGTGAC 60  
 Db 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
 QY 61 AAGTCCCAAAAGCAACTACTTGTACAACTACCTGCTCCAGCCCGGGCGGAGTACGGAC 120  
 Db 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 QY 121 TGCAGGAGTGTGAGAGCGCTCTTACCGCTTCAGAAACACCTCAGACACCTGCTC 180  
 Db 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 QY 181 AGCTGCTCCAAATGCGAAAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 240  
 Db 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 QY 241 CCGGACACCGGTGTGGCTGCAPCAAAGCAATAGAAATATTTGAGAGAAAAAT 300  
 Db 81 ArgAspThrValCysGlyCysArgLysGlnValGluIleSerSerCysThrValAsp 100  
 QY 301 TTCAGTGTCTTCAATTCAGCGCTCTGCTCAATGCACTTCACTCTCTCTCTCTCT 360  
 Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 QY 361 AAACAGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 QY 421 TCCTGTAGTAACTGTAAGAAAGCTGAGTGCAGAGTTGTGCTTACCCGATTTGAG 480  
 Db 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 QY 481 AAT 483  
 Db 161 Asn 161

## RESULT 4

US 09-899-422-4  
 ; Sequence 4, Application US/09899422  
 ; Patent No. US2002090676A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hauptmann, Rudolph  
 ; APPLICANT: Himmeler, Adolph  
 ; APPLICANT: Maurer-Foody, Ingrid  
 ; APPLICANT: Stratawa, Christian  
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 ; TITLE OF INVENTION: Them

; FILE REFERENCE: 98,385-H  
 ; CURRENT APPLICATION NUMBER: US/09/899,422  
 ; CURRENT FILING DATE: 2001-08-21  
 ; PRIOR APPLICATION NUMBER: 09/525,998  
 ; PRIOR FILING DATE: 2000-03-15  
 ; PRIOR APPLICATION NUMBER: 08/383,676  
 ; PRIOR FILING DATE: 1995-02-01  
 ; PRIOR APPLICATION NUMBER: 08/153,287  
 ; PRIOR FILING DATE: 1993-11-17  
 ; PRIOR APPLICATION NUMBER: 07/821,750  
 ; PRIOR FILING DATE: 1992-01-02  
 ; PRIOR APPLICATION NUMBER: 07/511,430  
 ; PRIOR FILING DATE: 1990-04-20  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 161  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-899-422-4

Alignment Scores:  
 Pred. No.: 4 38e-80 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-882-735-1 (1-483) x US-09-899-422-4 (1-161)  
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 Db 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
 QY 61 AAGTCCCAAAAGCAACTACTTGTACAACTACCTGCTCCAGCCCGGGCGGAGTACGGAC 120  
 Db 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 QY 121 TGCAGGAGTGTGAGAGCGCTCTTACCGCTTCAGAAACACCTCAGACACCTGCTC 180  
 Db 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 QY 181 AGCTGCTCCAAATGCGAAAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 240  
 Db 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 QY 241 CCGGACACCGGTGTGGCTGCAPCAAAGCAATAGAAATATTTGAGAGAAAAAT 300  
 Db 81 ArgAspThrValCysGlyCysArgLysGlnValGluIleSerSerCysThrValAsp 100  
 QY 301 TTCAGTGTCTTCAATTCAGCGCTCTGCTCAATGCACTTCACTCTCTCTCTCTCT 360  
 Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 QY 361 AAACAGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 QY 421 TCCTGTAGTAACTGTAAGAAAGCTGAGTGCAGAGTTGTGCTTACCCGATTTGAG 480  
 Db 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 QY 481 AAT 483  
 Db 161 Asn 161

## RESULT 5

US-09-907-263-2  
 ; Sequence 2, Application US/09907263  
 ; Patent No. US2002011924A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bendele, Alison M.

```

1 Senello, Regina M.
2 Edwards, Carl K.
3 TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
4 PROTEIN FOR TREATING TNF-MEDIATED DISEASES
5 NUMBER OF SEQUENCES: 4
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Amgen Inc.
8 STREET: 1840 DeHavilland Drive
9 City: Thousand Oaks
10 STATE: CA
11 COUNTRY: US
12 ZIP: 91320-1789
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patentin Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/907,263
20 FILING DATE: 17 Jul. 2001
21 CLASSIFICATION: <Unknown>
22 PRIORITY APPLICATION DATA:
23 APPLICATION NUMBER: US 09/326,394
24 FILING DATE: 1999-06-04
25 APPLICATION NUMBER: US 60/036,355
26 FILING DATE: 23-JAN-1997
27 APPLICATION NUMBER: US 60/039,315
28 FILING DATE: 07 FEB 1997
29 APPLICATION NUMBER: US 60/052,023
30 FILING DATE: 09-JUL-1997
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Zirdick, Thomas K.
33 REGISTRATION NUMBER: 32,185
34 REFERENCE/DOCKET NUMBER: A-430D
35 INFORMATION FOR SEQ ID NO. 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 161 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41 SEQUENCE DESCRIPTION: SEQ ID NO. 2
42
43 US-09-907-263 2
44
45 Alignment Scores:
46 Pred. No.: 4,38e-80 Length: 161
47 Score: 941.00 Matches: 161
48 Percent Similarity: 100.00% Conservative: 0
49 Best Local Similarity: 100.00% Mismatches: 0
50 Query Match: 100.00% Indels: 0
51 DB: 10 Gaps: 0
52
53 US-09-907-735 1 (1.483) X US-09-907-263 -2 (1.161)
54
55 Y Y 1 GATAGTGTGTGTCGCCAAGAAATAATATTCACCGCTCAAAATATTCGATTGGCTGACC 60
56 1 AsperseValcysproGlnGlyLysTyrIleHisproGlnAsnAsnSerIleCyscysThr 20
57 1 AAGAGCAAAAGAAAGCAAGCTATCTTGAACAATGATGTCACAGCGCGGAGAGAGAGAG 120
58 21 LyscysHisLysGlyThrTyrIleuTyrAsnAspCysproGlyproGlnAspThrAsp 40
59 121 TCAAGGAGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
60 41 CysArgGlnGlyLysGlnSerIlePheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60
61 191 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
62 61 SerCysSerLysCysArgLysGlnLeuGlnAlaGlnIleSerSerCysThrValAsp 80
63 241 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
64 81 ArgAspThrValCysGlnCysArgLysAsnGlnIleArgHisTyrIleTipSerGlnAsnLeu 100

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QY	301	TTCCAGTCCCTCAATTGACGCTCTGCGTCAATGGAGCCGTCACCTCTCCGCGCAGAG	360
Db	101	PheGlnCysPheAlaCysSerLeuCysLeuAlaGlyThrValHisLeuSerCysGlnIleu	120
QY	361	AAACAGAAACACCCGTGTACCCCTCCCATGACGTTCTTTCTTAAACAGAAACCAAGTGTCTC	420
Db	121	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal	140
QY	421	TTCGCTAGTACTGTAAAGAAACCGGAGGTGACAGAACTGTGGCTGCCAGATTGAG	480
Db	141	SerCysSerAlaCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGlu	160
QY	481	AAT 483	
Db	161	Asn 161	
RESULT 6			
US-09-899-429A-6			
/ Sequence 6, Application US/09899429A			
/ Patent No. US20020169118A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Hauptmann, Rudolph			
/ APPLICANT: Hummel, Adolph			
/ APPLICANT: Maurer-Fogy, Ingrid			
/ APPLICANT: Stratos, Christian			
/ TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for			
/ TITLE OF INVENTION: Them			
/ FILE REFERENCE: 98-385-J			
/ CURRENT APPLICATION NUMBER: US/09/899,429A			
/ CURRENT FILING DATE: 2001-07-03			
/ PRIOR APPLICATION NUMBER: 09/352,356			
/ PRIOR FILING DATE: 2000-02-23			
/ PRIOR APPLICATION NUMBER: 08/477,639			
/ PRIOR FILING DATE: 1995-06-07			
/ PRIOR APPLICATION NUMBER: 08/383,676			
/ PRIOR FILING DATE: 1995-02-01			
/ PRIOR APPLICATION NUMBER: 08/153,287			
/ PRIOR FILING DATE: 1993-11-17			
/ PRIOR APPLICATION NUMBER: 07/821,750			
/ PRIOR FILING DATE: 1992-01-02			
/ PRIOR APPLICATION NUMBER: 07/511,430			
/ PRIOR FILING DATE: 1990-04-20			
/ NUMBER OF SEQ ID NOS: 97			
/ SOFTWARE: PatentIn Ver. 2.0			
/ SEQ ID NO 6			
/ LENGTH: 162			
/ TYPE: PRT			
/ ORGANISM: Artificial Sequence			
/ FEATURE:			
/ OTHER INFORMATION: Description of Artificial Sequence: recombinant			
/ OTHER INFORMATION: TNF-BP sequence			
US-09-899-429A-6			
Alignment Scores:			
Pred. No.: 4,39e-80 Length: 162			
Score: 941.00 Matches: 161			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 9 Gaps: 0			
US-09-882-735-1 (1-483) X US-09-899-429A-6 (1-162)			
QY	1	GATAGTGTGATCCCAAGAAATATATCCACCCCAAAATATATGATTTGCTGATCC	60
Db	2	AspSerValCysProGlnGlnLysThrIleHisProGlnAsnAsnSerIleCysCysThr	21
QY	61	AAGTCCACAAAGAAACCTTACTGTATCAATGACTGTCCAGGCCCGGAGCAGATACGAC	120
Db	22	LysCysHisLysGlnThrIleuThrAsnAspCysProGlnPProGlnAspThrAsp	41
QY	121	TGCAGGAGATGTAGAGCGGCTCTCCACCGCTTGAGAAACACACTTAGACACTGCTC	180







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; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-10

Alignment Scores:
Pred. No.: 4-5e-80 Length: 183
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-882-735-1 (1-483) x US-09-899-429A-10 (1-183)
QY 1 GATAGTGTGTGTCCTCCCAAGSAAATATATATCCAGCTCAAAAATAATTCATTTCTCTGTAAG 60
DB 13 AspSerValCysProGlnGlyLysTyrIleHisProGlnAenAsnSerIleCysCysThr 32
QY 61 AAGTGCACAAAGAACTTACTTGTACAAATGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 33 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 52
QY 121 TGCAGSAGTGTGAGAGGCGGCTCTCTTCACGGTCTTCAAGAAACACCTCAGACACTGCCTC 180
DB 53 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 72
QY 181 AGTGTGTCCAAATGCGGAAAGAAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 73 SerCysSerLysCysArgLysGluMetGlyGlnValGluHisSerCysThrValAsp 42
QY 241 CGGACACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 93 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 112
QY 301 TTCAGTGTGTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 113 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 132
QY 361 AAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 420
DB 133 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 152
QY 421 TCCTGTAGTAGTAACCTGTGAGAAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 480
DB 153 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 172
QY 481 AAT 483
DB 173 Asn 173

RESULT 12
US-09-899-429A-18
; Sequence 18, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/183,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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1 PRIOR FILING DATE: 1992-07-02
2 PRIOR ART: "Art. 6, COMBET - 7/87", 410
3 PRIOR FILING DATE: 1990-04-20
4 NUMBER OF SEQ ID NOS: 97
5 SOFTWARE: PatentIn Ver. 2.0
6 SEQ ID NO: 18
7 LENGTH: 190
8 TYPE: PRT
9 ORGANISM: Artificial Sequence
10 FEATURE:
11 OTHER INFORMATION: Description of Artificial Sequence: recombinant
12 OTHER INFORMATION: tm bp sequence
13 JS-09-899 429A-18

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Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
PRIOR FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 201  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-14

Alignment Scores:  
Pred. No.: 4,6e-80 Length: 201  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-882-735-1 (1-483) X US-09-899-429A-14 (1-201)  
QY 1 GATAGTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 60  
DB 41 AspSerValCysProGlnGlyLysThrLeuAsnSerIleCysCysThr 60  
QY 61 AAGTGCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 120  
DB 61 LysCysHisGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
QY 121 TATAGTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 180  
DB 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
QY 181 AGTGTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 240  
DB 101 SerCysSerLysCysArgGluMetGlyGlnValGluLeuSerSerCysThrValAsp 120  
QY 241 CAGACACGCTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 300  
DB 121 ArgAspThrValCysArgGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 140  
QY 301 TTGACTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 360  
DB 141 PheGlnCysPheAsnGlySerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160  
QY 361 AAACAGAAATGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 420  
DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuLeuGluAsnGluCysVal 180  
QY 421 TGTGTAGTAACTTAAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 480

Db 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnLeu 200  
QY 481 AAT 483  
Db 201 Asn 201  
RESULT 15  
US-09-899-429A-8  
Sequence 8, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
PRIOR FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 8  
LENGTH: 211  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-8  
Alignment Scores:  
Pred. No.: 4,6e-80 Length: 211  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-882-735-1 (1-483) X US-09-899-429A-8 (1-211)  
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QY 61 AAGTGCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 120  
DB 61 LysCysHisGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80  
QY 121 TATAGTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGCTGACC 180  
DB 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
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DB 121 ArgAspThrValCysArgGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 140

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Page 10

[illegible]

Search completed: January 6, 2003, 03:47:38  
Job time : 33.5 secs

GenCore version 5.1.3  
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OW nucleic - protein search, using frame\_plus\_nzp model

Run on: January 6, 2003, 03:02:28 ; Search time 25 Seconds  
(without alignments)  
3714.634 Million cell updates/sec

Title: US-09-882-735-1  
Perfect score: 941  
Sequence: 1 gatagtggtgcccccaagg gctaccacagatggagaat 483

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Fgapop 6 0 , Fgapext 7 0  
Delop 6 0 , Delext 7 0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database: PIP\_73.4  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	941	100.0	455	1 GQHUT1	tumor necrosis fac
2	716.5	76.1	461	2 JG4302	tumor necrosis fac
3	680	72.3	454	1 GQSTT1	tumor necrosis fac
4	669	71.1	461	1 GQSTT1	tumor necrosis fac
5	187.5	19.9	435	2 154182	tumor necrosis fac
6	182.5	19.4	427	1 GQHUN	nerve growth facto
7	181	19.2	474	2 B38634	tumor necrosis fac
8	179.5	19.1	326	1 GQV2ML	T2 protein - myxom
9	178	18.9	325	2 B43692	T2 protein - rabbi
10	176.5	18.8	425	1 A36431	nerve growth facto
11	176	18.7	459	2 148854	gene murine tumour
12	167.5	17.8	305	2 A46476	B cell-associated
13	166.5	17.7	349	2 D72175	G protein - vari
14	164	17.4	348	2 T38623	hypothetical prote

## ALIGNMENTS

### RESULT 1

#### GQHUT1

tumor necrosis factor receptor 1 precursor [validated] - human  
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1  
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 Sequence revision 30-Jun-1992 #text change 08-Dec-2003  
C:Accession: A38208, A34899, A34960, A36555, C36555, A38281, G32027, J07098, A60.41, A60.42, A60.43, A60.44, A60.45, A60.46, A60.47, A60.48, A60.49, A60.50, A60.51, A60.52, A60.53, A60.54, A60.55, A60.56, A60.57, A60.58, A60.59, A60.60, A60.61, A60.62, A60.63, A60.64, A60.65, A60.66, A60.67, A60.68, A60.69, A60.70, A60.71, A60.72, A60.73, A60.74, A60.75, A60.76, A60.77, A60.78, A60.79, A60.80, A60.81, A60.82, A60.83, A60.84, A60.85, A60.86, A60.87, A60.88, A60.89, A60.90, A60.91, A60.92, A60.93, A60.94, A60.95, A60.96, A60.97, A60.98, A60.99, A60.100, A60.101, A60.102, A60.103, A60.104, A60.105, A60.106, A60.107, A60.108, A60.109, A60.110, A60.111, A60.112, A60.113, A60.114, A60.115, A60.116, A60.117, A60.118, A60.119, A60.120, A60.121, A60.122, A60.123, A60.124, A60.125, A60.126, A60.127, A60.128, A60.129, A60.130, A60.131, A60.132, A60.133, A60.134, A60.135, A60.136, A60.137, A60.138, A60.139, A60.140, A60.141, A60.142, A60.143, A60.144, A60.145, A60.146, A60.147, A60.148, A60.149, 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A60.1134, A60.1135, A60.1136, A60.1137, A60.1138, A60.1139, A60.1140, A60.1141, A60.1142, A60.1143, A60.1144, A60.1145, A60.1146, A60.1147, A60.1148, A60.1149, A60.1150, A60.1151, A60.1152, A60.1153, A60.1154, A60.1155, A60.1156, A60.1157, A60.1158, A60.1159, A60.1160, A60.1161, A60.1162, A60.1163, A60.1164, A60.1165, A60.1166, A60.1167, A60.1168, A60.1169, A60.1170, A60.1171, A60.1172, A60.1173, A60.1174, A60.1175, A60.1176, A60.1177, A60.1178, A60.1179, A60.1180, A60.1181, A60.1182, A60.1183, A60.1184, A60.1185, A60.1186, A60.1187, A60.1188, A60.1189, A60.1190, A60.1191, A60.1192, A60.1193, A60.1194, A60.1195, A60.1196, A60.1197, A60.1198, A60.1199, A60.1200, A60.1201, A60.1202, A60.1203, A60.1204, A60.1205, A60.1206, A60.1207, A60.1208, A60.1209, A60.1210, A60.1211, A60.1212, A60.1213, A60.1214, A60.1215, A60.1216, A60.1217, A60.1218, A60.1219, A60.1220, A60.1221, A60.1222, A60.1223, A60.1224, A60.1225, A60.1226, A60.1227, A60.1228, A60.1229, A60.1230, A60.123



R;Satoh, B.; Pauli, U.  
 Gene 163, 263-266, 1995  
 A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor  
 A:Reference numbers: J04302, MUID:96011645, PMID:7590278  
 A:Accession: J04302  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SUT>  
 A:Cross-references: GB:019994; NID:g1141752; PIDN:AA04849.1; PID:g1141753  
 A:Accession: PC4093  
 A:Molecule type: protein  
 A:Residues: 1-7 <SU2>  
 A:Experimental source: kidney cell line 15  
 C:Genetics:

A:Gene: tnfr  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
 F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
 F:44-82/Domain: NGF receptor repeat homology <NG1>  
 F:84-126/Domain: NGF receptor repeat homology <NGF>  
 F:211-231/Domain: transmembrane #status predicted <TM>  
 F:161-447/Domain: signal transduction #status predicted <SIT>  
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 1.69e-53 Length: 461  
 Score: 716.50 Matches: 120  
 Percent Similarity: 85.16% Conservative: 12  
 Best Local Similarity: 77.42% Mismatches: 22  
 Query Match: 76.14% Indels: 1  
 Gaps: 2  
 DB:

US 09 882-735-1 (1-481) x J04302 (1-461)

QY 1 GAAAGTGTGTGTTTAAAGGAAATATATACACCTCAAAATATTCATTGTGTGATCC 60  
 PB 41 GluSerLeuCysProGlnGlyTyrSerHisProGlnAsnArgSerIleCysCysThr 60  
 QY 61 AACTGCGCAAAAGCAACTTCTTACAAATGACTGTCTCCACCGCGGCGGACGATACGGAC 120  
 PB 61 LysCysHisLysGlyThrTyrLeuHisAsnAspCysLeuGlyProGlyLeuAspThrAsp 80  
 QY 121 TCAAGGAGTTCAGACGGGTCTCTTCAAGGTTCTAGAAAACCACTCAGACACTGGCTC 180  
 PB 81 CysArgGlyCysAspAsnGlyThrPheThrAlaSerGluAsnHisLeuThrGlnCysLeu 100  
 QY 181 AATATATCAAAATCAAGAAACAAATGATTCAGGTGAGATCTCTTTCACAGTGGAC 240  
 PB 101 SerCysSerLysCysArgSerGluMetSerGlnValGluIleSerProCysThrValAsp 120  
 QY 241 CAGGAAACGATTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
 PB 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgLysTyrTrpSerGluThrLeu 140  
 QY 301 TTCAGTGTGTTTAATTGAGGTTTCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 PB 141 PheGlnCysLeuAsnSerLeuCysProAsnGlyThrValGlnLeuProCysLeuGlu 160  
 QY 361 AAACAAACGAGTGTGCACTGCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
 PB 161 LysGlnAspThrLysCysAsnCysHisSerGlyPhePheLeuArgAspLysGlyCysVal 180  
 QY 421 TCTTATATTAATTTAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 485  
 PB 181 SerCysValAsnCysLysAsnAla--AspCysLysAsnLeuCys 194

RESULT 3

Q05M11

N:Alternate names: tumor necrosis factor precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10 Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 01-Dec-2000

C:Accession: A38634; B40254; S16677; S19031; I54332; I57824  
 R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wozniak, G.H.W.; Chen, E.  
 Proc Natl Acad Sci U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
 A:Reference numbers: A38634, MUID:91187885, PMID:1849278  
 A:Accession: A38634  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <LEW>  
 A:Cross-references: GB:M60468, NID:g199825; PIDN:AAA19751.1; PID:g199826  
 R;Goodwin, P.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.L.; Copeland, N.G.; Jenk  
 Mol Cell Biol 11 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A:Reference numbers: A40254, MUID:9146168, PMID:1645445  
 A:Accession: B40254  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <GO2>  
 A:Cross-references: GB:M60468, NID:g199825; PIDN:AAA19751.1; PID:g199826  
 R;Barrett, K.; Taylor-Fishwick, P.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Polman  
 Eur J Immunol 21, 1649-1656, 1991  
 A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis  
 A:Reference numbers: S16677, MUID:91285014, PMID:1649956  
 A:Accession: S16677  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <BAR>  
 A:Cross-references: EMBL:X59238, NID:g33578; PIDN:CAA11922.1; PID:g54579  
 R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.  
 Immunogenetics 34, 338-340, 1991  
 A:Title: Molecular cloning and expression of the mouse Tnf receptor type b  
 A:Reference numbers: S19021, MUID:92039815, PMID:1657766  
 A:Accession: S19021  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <ROT>  
 A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA00936.1; PID:g54849  
 R;Bebo, B.F.  
 Immunogenetics 39, 450-451, 1994

A:Title: Nucleotide sequence of the TNF type 1 receptor from a mouse endothelioma cell line  
 A:Reference numbers: I54532, MUID:9445232, PMID:8188324  
 A:Accession: I54532  
 A:Status: translated from GB/EMBL/DDAJ  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <RES>  
 A:Cross-references: GR:I26349; NID:g430732; PIDN:AAA59361.1; PID:g430733  
 R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.  
 Mol Immunol 30, 165-176, 1993  
 A:Title: Genomic organization and promoter function of the murine tumor necrosis factor  
 A:Reference numbers: I57826; MUID:93156721; PMID:8181516  
 A:Accession: I57826

A:Status: preliminary, translated from GB/EMBL/DDAJ  
 A:Molecule type: DNA  
 A:Residues: 1-393, G', 395-454 <RE2>  
 A:Cross-references: GB:M76656, NID:g202100; PIDN:AAA0465.1; PID:g202102  
 C:Comment: This protein is one of two distantly related receptors for both TNF alpha (cd

C:Genetics:  
 A:Gene: TNFR-2  
 A:Introns: 13/3, 65/1, 108/1, 158/1, 184/2, 210/1, 248/1, 257/3, 271/1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
 F:30-212/Domain: extracellular #status predicted <EXT>  
 F:44-82/Domain: NGF receptor repeat homology <NG1>  
 F:44-126/Domain: NGF receptor repeat homology <NG2>  
 F:127-167/Domain: NGF receptor repeat homology <NG3>  
 F:168-204/Domain: NGF receptor repeat homology <NG4>  
 F:213-235/Domain: transmembrane #status predicted <MEM>  
 F:236-454/Domain: intracellular #status predicted <INT>  
 F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 2.26e-50 Length: 454  
 Score: 680.00 Matches: 112  
 Percent Similarity: 83.44% Conservative: 19  
 Best Local Similarity: 71.34% Mismatches: 26

Query Match: 72.26% Indels: 0  
DB: 1 Gaps: 0  
US-09-882-735-1 (1-483) x GOMST1 (1-454)

QY 1 GATATGTTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTTGCTGTACC 60  
DB 1 ASPSERLEUCYSPROGLINGLYSTYRVALHISERLYSASNAHSERILECYSTYR 60  
QY 61 AAGTCCCAAAAGAACCTTACTTGATGATGCTCCAGGCCCGGGGAGAGATACGAC 120  
DB 61 LYSCTSHLSYSGLYTHRTYRLEUVALSERASPYSERPROGLYGLNGLNTHRVAL 80  
QY 121 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACACCTGACACTGCTTC 180  
DB 81 CYSAGTGLUCYSGLYTHRTYRLEUVALSERGLNGLNTHRVALSERGLNGLNTHR 100  
QY 181 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGGAGATCTTCTTGCACAGTGCAC 240  
DB 101 SERCYSLYSTRHCYSARGLYSGLMETSERGLNGLNTHRVALSERPROCYSGLNALASP 120  
QY 241 CGGACACCGTGTGTGCTGCTGCTGCTCAATGGGACCGGCAATTATGGAGTGAACCTT 300  
DB 121 LYSASPHTHRVALCYSGLYCYSLYSASNGLNPHGLNARGTYRLEUVALSERGLNTHR 140  
QY 301 TTCCAGTCTTCAATTGACGCTCTGCTCAATGGGACCGGCACTTCTCTGCGCAGAG 360  
DB 141 PHEGLNLYSVALASPYSSERPROCYSPHEASNGLYTHRVALTHRTLEPROCYSLYSGLN 160  
QY 361 AAACGAAACCGGTGTCACCTGCTGCTGCTCAATGGGACCGGCACTTCTTCTTAAAGAAACGAGTGTG 420  
DB 161 THRGINSHTHRVALCYASNCYSHLSAAGLYPHEPHELEUVALSERGLNGLNTHR 180  
QY 421 TCCTGTAGTAACTGTAAAGAAACCTGAGTGCACGAGTTGTGCTTACCC 471  
DB 181 PROCYSSERHISCYSLYSASNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 197

RESULT 4  
GORITL  
tumor necrosis factor receptor 1 precursor - rat  
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
C:Accession: B16555  
R:Hammer, A., Maier, F., Krenke, Y., Scheurich, P., Pfizenmaier, K., Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990  
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
A:Reference number: A36555, MUID:91090841, PMID:1702293  
A:Accession: B36555  
A:Molecule type: mRNA  
A:Residues: 1-461 <HM>  
A:Cross-references: GB:M63122, MID:g207361, PIDN:AAA4256.1, PID:g207362  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: duplication, glycoprotein; receptor; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F:30-211/Domain: extracellular #status predicted <EXT>  
F:30-203/Product: tumor necrosis factor binding protein #status predicted <TRP>  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-234/Domain: NGF receptor repeat homology <NG4>  
F:235-461/Domain: intracellular #status predicted <INT>  
F:54-151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 1,97e-49 Length: 461  
Score: 669.00 Matches: 110  
Percent Similarity: 79.50% Conservative: 18  
Best Local Similarity: 68.32% Mismatches: 33  
Query Match: 71.09% Indels: 0

DB: 1 Gaps: 0  
US-09-882-735-1 (1-483) x GORIT1 (1-461)

QY 1 GATATGTTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTTGCTGTACC 60  
DB 41 ASPSERLEUCYSPROGLINGLYSTYRVALHISERLYSASNAHSERILECYSTYR 60  
QY 61 AAGTCCCAAAAGAACCTTACTTGATGATGCTCCAGGCCCGGGGAGAGATACGAC 120  
DB 61 LYSCTSHLSYSGLYTHRTYRLEUVALSERASPYSERPROGLYGLNGLNTHRVAL 80  
QY 121 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACACCTGACACTGCTTC 180  
DB 81 CYSAGTGLUCYSGLYTHRTYRLEUVALSERGLNGLNTHRVALSERGLNGLNTHR 100  
QY 181 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGGAGATCTTCTTGCACAGTGCAC 240  
DB 101 SERCYSLYSTRHCYSARGLYSGLMETSERGLNGLNTHRVALSERPROCYSGLNALASP 120  
QY 241 CGGACACCGTGTGTGCTGCTGCTGCTCAATGGGACCGGCAATTATGGAGTGAACCTT 300  
DB 121 LYSASPHTHRVALCYSGLYCYSLYSASNGLNPHGLNARGTYRLEUVALSERGLNTHR 140  
QY 301 TTCCAGTCTTCAATTGACGCTCTGCTCAATGGGACCGGCACTTCTCTGCGCAGAG 360  
DB 141 PHEGLNLYSVALASPYSSERPROCYSPHEASNGLYTHRVALTHRTLEPROCYSLYSGLN 160  
QY 361 AAACGAAACCGGTGTCACCTGCTGCTGCTCAATGGGACCGGCACTTCTTCTTAAAGAAACGAGTGTG 420  
DB 161 THRGINSHTHRVALCYASNCYSHLSAAGLYPHEPHELEUVALSERGLNGLNTHR 180  
QY 421 TCCTGTAGTAACTGTAAAGAAACCTGAGTGCACGAGTTGTGCTTACCC 480  
DB 181 PROCYSSERHISCYSLYSASNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 200

RESULT 5  
154182  
tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: U54182  
R:Baens, M.; Chalfant, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.;  
Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen  
A:Reference number: U54182, MUID:9352381, PMID:8486360  
A:Accession: U54182  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Cross-references: GDB:1230195, OMIM:600979  
A:Map position: 12p13.3-12p13.1  
C:Superfamily: tumor necrosis factor receptor type 1, NGF receptor repeat homology

Alignment Scores:  
Pred. No.: 3,29e-08 Length: 435  
Score: 187.50 Matches: 49  
Percent Similarity: 44.00% Conservative: 17  
Best Local Similarity: 32.67% Mismatches: 71  
Query Match: 19.93% Indels: 13  
DB: 2 Gaps: 7

US-09-882-735-1 (1-483) x U54182 (1-435)

QY 22 AATATATTCACCTCAAAATATATGATTTGCTGTACCAAGTGCACAAAGAACCTAC 81  
DB 22 AATATATTCACCTCAAAATATATGATTTGCTGTACCAAGTGCACAAAGAACCTAC 81







Db 207 ThrAsp---CysAspPro 211  
 RESULT 9  
 B43692  
 T2 protein - rabbit fibroma virus  
 C:Species: rabbit fibroma virus, Shope fibroma virus  
 C:Date: 10-Sep-1993 #sequence\_revision 30 Sep 1993 #text\_change 07-May-1999  
 C:Accession: B43692  
 R:Upton, C.; DeLange, A.M.; McFadden, G  
 Virology 160, 20-30, 1997  
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
 A:Reference number: A43692; MUID:87321103; PMID:2820128  
 A:Accession: B43692  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-325 <UPT>  
 A:Cross references: GB:M17433  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:64-105/Domain: NGF receptor repeat homology <NG2>  
 F:106-147/Domain: NGF receptor repeat homology <NG3>  
 Alignment Scores:  
 Pred. No.: 2-246-07 Length: 325  
 Score: 178.00 Matches: 45  
 Percent Similarity: 39.47% Conservative: 15  
 Best Local Similarity: 29.61% Mismatches: 62  
 Query Match: 18.92% Indels: 30  
 DB: 2 Gaps: 6  
 US 09 882 735-1 (1-483) x B43692 (1-325)  
 QY 37 CAATAATTCATTGCTGTACCAAGTGGCCAAAGAACCTACTGTCAATGACTGT 96  
 Db 34 GtLUyAspGlyLeuCySerCysAlaSerCysHisProGlyPheTyAlaSerArgLeuCyS 53  
 QY 97 TCAAGT 156  
 Db 54 --- GlyProGlySerAsnThrValCySerProCySArgValCySAsnCySerThrGlyAsn 72  
 QY 157 GAAACACACCTCAGACCTGCTTACCTGCTTACCTGCTTACCTGCTTACCTGCTTAC 213  
 Db 73 ThrAsnHisAlaProAlaCysValSerCysArgGlyProCySThrGlyHisLeuSer--- 91  
 QY 214 GTGACATCTCTTCTGTACAGTGCACGGACACACGCTGTGTGTGTGTGTGTGTGTGT 273  
 Db 92 --- GluSerGlnProCySAspArgThrHisAspArgValCySAsnCySerThrGlyAsn 110  
 QY 274 TACCGGACATTATTCAGTCAAAACCTTTTCCAGTGTCTTCAATTGCAGCTCTGCCTCA 333  
 Db 111 TyrCysLeuLeuGlyGlyGlnAsn-----GlyCysArgIleCysAlaPro 125  
 QY 334 GGCACCGGTGACCTTCTGT 393  
 Db 126 GlnThr-----LysCysProAlaGly 132  
 QY 394 TTCTTTTCAACAAACAGT 441  
 Db 133 TyrGlyValSerGlyHisThrArgAlaGlyAspThrLeuCySGLuLySpsProHis 152  
 QY 442 -----AGCTGCAGTGCACGAGTGTGTC 465  
 Db 153 ThrTyrSerAspSerLeuSerProThrGluArgCys 164  
 RESULT 10  
 A26431  
 nerve growth factor precursor, low affinity - rat  
 N:Alternate names: NGF receptor  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10 Sep 1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A26431; PH1229  
 R:Radake, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
 Nature 325, 593-597, 1987  
 A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A:Reference number: A26431; MUID:87115859; PMID:4027580  
 A:Accession: A26431  
 A:Molecule type: mRNA  
 A:Residues: 1-425 <RAD>  
 A:Cross references: GB:X05137; NID:956755; PION:CAA28781.1; PH1229-6756  
 R:Metsis, M.; Timmusk, T.; Allikmets, P.; Saarma, M.; Persson, H.  
 Gene 121, 247-254, 1992  
 A:Title: Regulatory elements and transcriptional regulation by testis-specific and testis-expressed genes  
 A:Reference number: PH1229; MUID:93077038; PMID:1446821  
 A:Accession: PH1229  
 A:Molecule type: DNA  
 A:Residues: 1-20 <MET>  
 A:Cross references: GB:X61269  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on the extracellular domain may form part or all of a high-affinity receptor when it associates with a ligand.  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates with a ligand.  
 C:Genetics: 20/3  
 A:Introns: 20/3  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; signal sequence; signal sequence #status predicted <SIG>  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-425/Product: nerve growth factor receptor #status predicted <MAT>  
 F:30-251/Domain: extracellular #status predicted <EXT>  
 F:33-66/Domain: NGF receptor repeat homology <NG1>  
 F:68-109/Domain: NGF receptor repeat homology <NG2>  
 F:110-148/Domain: NGF receptor repeat homology <NG3>  
 F:150-190/Domain: NGF receptor repeat homology <NG4>  
 F:198-249/Region: serine/threonine-rich  
 F:252-273/Domain: transmembrane #status predicted <MEM>  
 F:274-425/Domain: intracellular #status predicted <INT>  
 F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred No.: 2 896-07 Length: 425  
 Score: 176.50 Matches: 50  
 Percent Similarity: 46.30% Conservative: 25  
 Best Local Similarity: 30.86% Mismatches: 68  
 Query Match: 18.76% Indels: 19  
 DB: 1 Gaps: 10  
 US 09 882 735-1 (1-483) x A26431 (1-425)

QY 10 TGTCCTCCCAAGAAATATATATCCACCTCAAAATAATTGATTTCTCTTACCAAGTCA 69  
 Db 33 CysSerThrGlyLeuTyThrHis-----SerGlyGluCysCysLysAlaTyAsn 49  
 QY 70 AAGGAACTACTTGTCAATGACTGTCTGACGAGGAGAGATATGATATGATATGAT 129  
 Db 50 LeuGlyGluGlyValAlaGlnProCys---GlyAlaAsnGln---ThrValCysGluPro 67  
 QY 130 TGT---GAGACGGCTCCTTCAAGGCTTGTGAAAGGACCTTGTGACACTGCTGCTG 186  
 Db 68 CysLeuAspAsnValThrPheSerAspValValSerAlaThrGluProCysLysProCys 87  
 QY 187 TCCAAATGCCAAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243  
 Db 88 ThrGluCys-----LeuGlyLeuGlnSerMetSerAlaProCysValGluAlaAsp 104  
 QY 244 GACACCGT 304  
 Db 105 AspAlaValCysArgCys-----AlaTyrGlyTyrTyrGlnAspGluGluThrGly 111  
 QY 304 CAGTGTCTTCAATTCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 Db 122 HisCysGluAlaCysSerValCysGluValGlySerGlyLeuValPheSerCysGlnAsp 141  
 QY 361 AAACAGACACCGT 428  
 Db 142 LysGlnAsnThrValCysGluCysProGluGlyThrTyrSerAspGluAlaAsnHis 161  
 QY 409 ---AACAGAGT 468  
 Db 162 ValAspProCysLeuProCysThrValCysGluAspThrGluArgGlnLeuAlaGlyCys 181







GenCore version 5.1.1.3  
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QM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 02:15:49, Search time 15.5 seconds  
(without alignments)

2584.912 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 941

Sequence: 1 gatagtgtgtccccaagg... gctacccagattgagaat 483

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame+ n2p\_model -DEV=xlh  
Q:/gen2/1/isp/psp/seq/1509982735/runat\_01012003\_073943\_15212/app\_query\_fastx\_1\_647  
DB=SwissProt\_40 -QWMT=fastran -SUFFIX=rsb -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
UNITS=bits START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45  
-DOCALIGN=200 -THP\_SCORE=pt -THP\_MAX=100 -THP\_MIN=0 -ALIGN=15 -MODE=LOCAL  
OUTWMT=pt -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
USER=1509982735 -e/n 1.1.4 @runat\_01012003\_073943\_15212 -NCPH=6 -ICPU=3  
NO\_XIPXY -NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
YGAPOP=10 YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	455	TR1A_HUMAN	P19438 homo sapien
2	716.5	76.1	461	TR1A_PIG	P50555 sus scrofa
3	680	72.3	454	TR1A_MOUSE	P25118 mus musculus
4	674.5	71.7	471	TR1A_BOVIN	O19131 bos taurus
5	669	71.1	461	TR1A_PAT	P22914 rattus norv
6	200.5	21.3	176	TR21_MOUSE	O9863 mus musculus
7	200.5	21.3	176	TR12_HUMAN	Q93038 h tumor nec
8	198.5	21.1	180	TR22_MOUSE	Q9862 mus musculus
9	187.5	19.9	435	TR13_HUMAN	P36941 homo sapien
10	182.5	19.4	427	TR16_HUMAN	P08138 homo sapien
11	181.5	19.3	417	TR16_MOUSE	O92041 mus musculus
12	181	19.2	474	TR1B_MOUSE	P25119 mus musculus
13	179.5	19.1	326	VT2_MYXVL	P29825 myxoma viru
14	178	18.9	325	VT2_SFVKA	P25943 Shope fibro
15	176.5	18.8	332	TRN6_PIG	O77736 sus scrofa
16	176.5	18.8	425	TR16_FAT	P07174 rattus norv
17	167.5	17.8	289	TRN5_MOUSE	P27512 mus musculus
18	167.5	17.8	415	TRN3_MOUSE	P50284 mus musculus

19	167	17.7	269	1	TRN5_BOVIN	Q28203 bos taurus
20	166.5	17.7	323	1	TRN6_BOVIN	P51667 bos taurus
21	166.5	17.7	349	1	CPMB_CAMPS	Q95477 campylobac vi
22	164	17.4	349	1	CPMB_VAPV	P34016 variola vir
23	164	17.4	351	1	CPMB_COWPX	O73659 cowpox viru
24	164	17.4	401	1	TL1B_HUMAN	O00460 homo sapien
25	162.5	17.3	327	1	TRN6_MOUSE	P25444 mus musculus
26	161	17.1	461	1	TR1B_HUMAN	P20433 homo sapien
27	158	16.8	401	1	TL1B_PAT	O08727 rattus norv
28	154	16.4	401	1	TL1B_MOUSE	O98712 mus musculus
29	147	15.6	324	1	TRN6_RAT	O63199 rattus norv
30	145	15.4	416	1	TR14_CHICK	P10419 gallus gall
31	142	15.1	283	1	TR14_HUMAN	O29556 homo sapien
32	141	15.1	386	1	TL03_HUMAN	O29556 homo sapien
33	141	15.0	1680	1	PUR2_DROME	P30432 drosophila
34	139.5	14.8	250	1	TRN7_MOUSE	P41272 mus musculus
35	139.5	14.8	277	1	TRN6_HUMAN	P26942 homo sapien
36	139	14.8	259	1	TL0C_HUMAN	O14798 h tumor nec
37	138.5	14.7	260	1	TRN7_HUMAN	P26842 homo sapien
38	137	14.6	440	1	TL0B_HUMAN	O14763 homo sapien
39	134	14.2	1696	1	PCF5_BPACL	O09115 branchiost
40	134	14.2	1877	1	PCF5_MOUSE	O04192 mus musculus
41	133	14.1	687	1	VS41_GIALA	P92127 giardia lum
42	132.5	14.1	655	1	TR11_MOUSE	O98741 mus musculus
43	132	14.0	913	1	PCF5_HUMAN	O92824 homo sapien
44	131.5	14.0	272	1	TRN4_MOUSE	P47741 mus musculus
45	130.5	13.9	335	1	TRN6_HUMAN	P25445 homo sapien

## ALIGNMENTS

RESULT 1  
TR1A\_HUMAN STANDARD; PRT; 455 AA.  
AC F19438;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-P1) (TNF-P1) (p55) (CD120a) [Contains Tumor necrosis factor  
DE binding protein 1 (TBPI)]  
GN TNFPSF1A OP TNFPI OP TNFAR  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=90235285; PubMed=2158863;  
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,  
RA Getanaga T., Granger G.A., Lentz R., Paab H., Kohn W.J., Goodell D.V.,  
RA "Molecular cloning and expression of a receptor for human tumor  
RT necrosis factor."  
RL Cell 61:361-370(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=30235284; PubMed=2158862;  
RX Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,  
RA Tabuchi H., Lesslauer W.,  
RT "Molecular cloning and expression of the human 55 kd tumor necrosis  
RT factor receptor."  
RL Cell 61:351-359(1990).  
RN [3]  
RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
RC MEDLINE=91006021; PubMed=1698610;  
RX Noppar Y., Kemper O., Brakelusch C., Engelmann H., Zwanq R.,  
RA Aderka D., Holmann H., Wallach D.,  
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA  
RT for the type I TNF-R, cloned using amino acid sequence data of its  
RT soluble form, encodes both the cell surface and a soluble form of the  
RT receptor."  
PL EMBO J 9 3269-3278(1990)

RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:91092841, PubMed:1702293;  
 RA Hantley A., Maurer-Pegib I., Kroenke M., Scheuch P., Pfizenmaier K.,  
 RA Lantz M., Olsson I., Hauptmann R., Stratos C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis  
 RT factor receptor chain (p60) and its soluble derivative, tumor  
 RT necrosis factor-binding protein.";  
 RL DNA Cell Biol 9:705-715(1990).  
 PL [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE:91017509, PubMed:2170974;  
 RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;  
 RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
 RT expression of recombinant soluble TNF-binding protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:92550049, PubMed:1151717;  
 RA Fuchs P., Strichl S., Dworzak M., Himmeler A., Ambros P.F.;  
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
 RT localization to chromosome 12p13.";  
 RL Genetics 13:219-224(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE:90110015, PubMed:2153136;  
 RA Engelmann H., Novick D., Malisch D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
 RX MEDLINE:93258809, PubMed:8387891;  
 RA Banner D.W., D'Arcy A., Jones W., Gentz P., Schenfeld H.J.,  
 RA Broger C., Loetscher H., Lesslauer W.;  
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 RT beta complex: implications for TNF receptor activation.";  
 RL Cell 73:431-445(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE:97094982, PubMed:8939750;  
 RA Natsmith J.H., Devine T.Q., Khono H., Sprang S.R.;  
 RT "Structures of the extracellular domain of the type I tumor necrosis  
 RT factor receptor.";  
 RL Structure 4:1251-1262(1996).  
 RN [11]  
 RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
 RX MEDLINE:99215501, PubMed:10194009;  
 RA McDermott M.F., Aksentjevich I., Galon J., McDermott E.M.,  
 RA Gunkelade B.W., Gentola M., Mansfield E., Gidina M., Karenko L.,  
 RA Petersson T., McCarthy J., Frucht D.M., Aringer M., Torosian Y.,  
 RA Tepo A.-W., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
 RA Schlimgen R., Kumarajewa T.P., Cooper S.M., Vella J.P., Amos C.I.,  
 RA Mulvey J., Chan K.A., Molloy M.G., Phaki A., Powell R.J.,  
 RA Hiltan G.A., O'Shea J., Kastner D.L.;  
 RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
 RT receptor, TNFR1, define a family of dominantly inherited  
 RT autoinflammatory syndromes.";  
 RL Cell 97:133-144(1999).  
 CC FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase 8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis. Contributes to  
 CC the induction of noncytotoxic TNF effects including anti-viral

CC state and activation of the acid sphingomyelinase.  
 CC -1 SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC -1 DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC -1 PTM: The soluble form is produced from the membrane form by  
 CC proteolytic processing.  
 CC DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
 CC familial hibernian fever (FHF), a disease characterized by  
 CC recurrent fever, abdominal pain, localized tender skin lesions and  
 CC myalgia.  
 CC -1 SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1 SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -1 DATABASE: NAME=PROM; NOTE=CD guide C0120a entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
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 CC -----  
 CC EMBL; X55313; CA93021.1; -  
 CC EMBL; M33294; AAA03210.1; -  
 CC EMBL; M58286; AAA36753.1; -  
 CC EMBL; M63121; AAA36754.1; -  
 CC EMBL; M75866; AAA61201.1; -  
 CC EMBL; M75864; AAA61201.1; JOINED.  
 CC EMBL; M73865; AAA61201.1; JOINED.  
 CC EMBL; M60275; AAA36756.1; -  
 CC EMBL; AC1522; CAA01558.1; -  
 CC EMBL; BC010140; AAH10140.1; -  
 CC PIR; A34899; GQHUT1.  
 CC PIR; A35010; A35010.  
 CC PIR; S12057; S12057.  
 CC PIR; A38208; A38208.  
 CC PDB; 1TNR; 31-JUL-94.  
 CC PDB; 1NCF; 07-DEC-95.  
 CC PDB; 1EXT; 11-JAN-97.  
 CC GeneW; HGNC:11916; TNFRSF1A.  
 CC MIM; 191190; -  
 CC MIM; 142680; -  
 CC InterPro; IPR000488; Death.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF00020; TNFR\_c6; 4.  
 CC Pfam; PFC0531; death; 1.  
 CC PRODOM; PD000771; TNFR\_c6; 1.  
 CC SMART; SM00005; DEATH\_1.  
 CC SMART; SM00208; TNFR; 4.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 3  
 CC PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
 CC PROSITE; PS00017; DEATH DOMAIN; 1.  
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
 CC Disease mutation; Polymorphism; 3d-structure.  
 CC SIGNAL  
 CC CHAIN 1 21  
 CC SIGNAL 22 455  
 CC CHAIN 41 291  
 CC DOMAIN 22 211  
 CC TRANSSEM 212 234  
 CC DOMAIN 235 455  
 CC REPEAT 43 82  
 CC REPEAT 83 125  
 CC TNFR-CYS 1.  
 CC TNFR-CYS 2.  
 CC TUMOR NECROSIS FACTOR RECEPTOR  
 CC SUPERFAMILY MEMBER 1A, MEMBRANE FORM.  
 CC TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC POTENTIAL.  
 CC CTOPOLASMIC (POTENTIAL).  
 CC TNFR-CYS 1.  
 CC TNFR-CYS 2.





FT CARGOHD 54 54 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARGOHD 86 86 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARGOHD 145 145 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARGOHD 151 151 N-LINKED (GLCNAC) (POTENTIAL)  
 SU SEQUENCE 461 AA, 50036 MW, 6273361E0C092D3 CRC64;

## Alignment Scores:

Pred. No.: 2 54e-57 Length: 461  
 Score: 716.50 Matches: 120  
 Percent Similarity: 85.16% Conservative: 12  
 Best Local Similarity: 77.43% Mismatches: 22  
 Query Match: 76.14% Indels: 1  
 Gaps: 1

US-09-882-735-1 (1-483) x TR1A\_PIG (1-461)

UY 1 GATAGTGTCTCTCCCAAGAAATATATACACCTGCAAAATATTCGATTGCTGAC 60  
 DB 41 GUSLEUCYSPROGINDLYSTYSETHSPROGINANAGSERILECYSGYTHR 60  
 UY 61 AAGIGCCACAAAGAACTACTTGTACATATCTCCUAGCCCGGCGAGATACGAC 120  
 DB 61 LYSCTSH:STYSGLYTHRTYLEUHSANASPCYLEUGLYPROGLYLEUASPTHRASP 80  
 UY 121 TCGAGGAGATGTGAGAGCGGCTCCCTTCACCGCTTCAGAAACCACTCAGACACTGCTC 180  
 DB 81 CYAAGGLUCYASPSANGLYTHRPHETHRILASERGLUASNHISLEUTHRGINCYSL 100  
 UY 141 AATCTCTTAAATCTCAAAATATATATATATATATATATATATATATATATATAT 240  
 DB 101 SERCTSELYCYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGY 120  
 UY 241 GAGGAGATGTGAGAGCGGCTCCCTTCACCGCTTCAGAAACCACTCAGACACTGCTC 300  
 DB 121 AATCTCTTAAATCTCAAAATATATATATATATATATATATATATATATATATAT 140  
 UY 361 TTTCTGATGTCTCTCCCAAGAAATATATATATATATATATATATATATATATATAT 360  
 DB 141 PHEGICYSLEASNCYSEILEUCYSPROKNGLYTHRTYLGIRLEPROCYSL 160  
 UY 361 AAGGAGATGTGAGAGCGGCTCCCTTCACCGCTTCAGAAACCACTCAGACACTGCTC 420  
 DB 161 LYSGLINAPHTLLECYASNYSHISSEIRLYPHEPHELEUAGASPLYSGLI 180  
 UY 421 TTTCTGATGTCTCTCCCAAGAAATATATATATATATATATATATATATATATATAT 465  
 DB 181 SERCTSELYCYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGYSGY 194

## RESULT 3

TR1A\_MOUSE STANDARD: PRT: 454 AA.

AC P25118, 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (p55).  
 GN TNFRSF1A OP TNFR1 OP TNFR-1.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Euteleostomi;  
 CC Eumetazoa; Eumetazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=918785; PubMed=1843278,  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wang G.H., Chen E.Y., Goeddel D.V.;  
 RA "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific";  
 PL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.

EX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor";  
 RT Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=91285014; PubMed=1647956;  
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissenerghis A.M.,  
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;  
 RA "Cloning, expression and cross-linking analysis of the murine p55  
 RT tumor necrosis factor receptor";  
 RT Eur. J. Immunol. 21:1649-1656(1991).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Spleen;  
 PC MEDLINE=92039815; PubMed=1657766;  
 RA Roche J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b";  
 RT Immunogenetics 34:338-340(1991).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=94245292; PubMed=8188324;  
 RA Bebo B.F., Linthicum D.S.;  
 RT "Nucleotide sequence of the TNF type I receptor from a mouse  
 RT endothelioma cell line";  
 RT Immunogenetics 39:450-451(1994).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=93156721; PubMed=8381516;  
 RA Roche J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 RT "Genomic organization and promoter function of the murine tumor  
 RT necrosis factor receptor beta gene";  
 RT Mol. Immunol. 30:165-175(1993).  
 RN [7]  
 RN SEQUENCE FROM N.A.  
 RP Strausberg R.;  
 RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (by similarity).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOOLIGERIZATION. ONCE ASSEMBLED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: M60468; AAA39751.1;  
 CC EMBL: M59377; AAA40464.1;  
 CC EMBL: X59238; AAA4922.1;  
 CC EMBL: X57796; CAA40936.1;  
 CC EMBL: L26349; AAA59361.1;  
 CC EMBL: M76656; AAA40465.1;  
 CC EMBL: M88067; AAA40465.1; JOINED.  
 CC EMBL: M76655; AAA40465.1; JOINED.



















RC STRAIN-A;  
RX MEDLINE=99077793; PubMed=9857182;  
RA Tuffreau C., Benejean J., Blondel P., Kieffer B., Flament A.;  
RT "Low affinity nerve-growth factor receptor (p75NTR) can serve as a  
RL receptor for rabies virus";  
CC EMBO J. 17:7250-7259(1998).  
CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,  
CC AND NT-4. Can mediate cell survival as well as cell death of  
CC neural cells (By similarity). Binds to rabies virus glycoprotein  
CC Gs.  
CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR  
CC associated cell death executor (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- PTM: N- AND O glycosylated (By similarity).  
CC -!- PTM: Phosphorylated on serine residues (By similarity).  
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

[illegible]





```

PA Bartling B., Hoffmann U., Holtz J., Schulte P., Hensch G., Tharmer D.,
RT "Expression of apoptosis-associated genes in hibernating and stunned
FL myocardium of pig";
CC Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs cascade of caspases
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 TNFR-DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CF EWEI, AJ031523, CACG4536.1, -.
DF HSSP, P25445, IDDP.
DF InterPro, IPRO00488; Death.
DF InterPro, IF001368, TNFR_C6.
CF EAM, IF001368, TNFR_C6; 3.
DR Pfam, PF00511; death; 1.
DR SMART, SMO0005; DEATH; 1.
DR SMART, SMO0208; TNFR; 3.
DE PROSITE, PS00552; TNFR_NSR_1, 2.
DE PROSITE, PS00550; TNFR_NGRF_2, 2.
DE PROSITE, PSS0017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT FT SIGNAL 1 16
FT CHAIN 17 332
FT TM 17 332
FT FM 17 332
FT FM TRANSMEM 176 192
FT FM DOMAIN 193 332
FT FM REPEAT 45 81
FT FM REPEAT 82 125
FT FM REPEAT 126 164
FT FM DOMAIN 227 311
FT FM DISULFID 46 57
FT FM DISULFID 58 71
FT FM DISULFID 61 80
FT FM DISULFID 83 99
FT FM DISULFID 102 117
FT FM DISULFID 105 125
FT FM DISULFID 127 141
FT FM DISULFID 144 155
FT FM DISULFID 147 163
FT FM CARBOHYD 38 38
FT FM CARBOHYD 116 116
SQ SEQUENCE 332 AA, 37592 MW, 58930368256B1B CRC64,
Alignment Scores:
pred.No.: 2,18e-08 Length: 332
Score: 176.50 Matches: 37
Percent Similarity: 43.31% Conservative: 18
Best Local Similarity: 29.13% Mismatches: 65
Query Match: 18.76% Indels: 7
D3: Gaps: 4
US-09-882-735-1 (1-463) x TNRF6_FIG (1-332)

```

```
Dh 43 GluSerGluCysProGluGlyGlnHis-----ArgGluGlyGlnPheCysCysGln 59
QY 61 AAGTGGACAAATGAACCTACTTGTACAATGACTGTCCAGGCGCGGCGAGATACGGAC 120
Dh 60 ProCysProGluGlyArgLysHisAlaAspCysThrSerProGlyGlyAlaProGln 79
QY 121 TGTACGGAGTTTTCAGAGGCGGCTTCTTCAACCGCTTCAGAAACCCACCTCAGACACTGC 177
Dh 80 CysValProCysSerGluGlyGluAspTyrThrAspLysAsnHisHisSerSerLysCys 99
QY 178 CTCAGTGTCTCCAAATGCCGAAGGAATGGGTGAGTGGAGATCTCTTCTTGACACAGTG 237
Dh 100 ArgArgCysArgValCysAspGlyGluHisGlyLeuGluValGluLysAsnCysThrArg 119
QY 238 GACGCGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 297
Dh 120 ThrGlnAsnThrLysCysArgCysLysProAsnPhePheCysHis-----ThrSerGln 137
QY 298 CTTTTCACATGTCTTAATTGAGCTTTTGTCTTAAATGCGACCGTGACCTCTCTCTGCCAG 357
Dh 138 CysGluHisCysAsnProCysThrThrCysGluHisGlyValIleGlu---AsnCysThr 156
QY 358 GACAAACAGACACACCGTGTGC 378
Dh 157 ProThrSerAsnThrLysCys 163
```

Search completed: January 6, 2003, 03:44:39  
Job time: 28.5 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM nucleic protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 01:17:59 ; Search time 51.5 Seconds  
(without alignments)

3864.884 Million cell updates/sec

Title: US-09-882 735 1

Perfect score: 941

Sequence: 1 qatagtgtgtccccaagg ... gctacccagattgagaat 483

Scoring table:

BLOSUM62  
Xgapop 10 0, Xgapext 0.5  
Ygapop 10 0, Ygapext 0.5  
Fgapop 6 0, Fgapext 7.0  
Delop 6 0, Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DR seq length: 0

Maximum DR seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame+.n2p.model -DEV=xih  
Q=/tmp/1/rspt0001/seq009882735/runat\_03012003\_073943\_15223/app\_query.fasta\_1.647  
DR-SPTREMBL\_21 -OPMT-fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=per -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
OUTFMT=ptc NPM-ext HEADLINE=500 MINLEN=0 MAXLEN=200000000  
USER-US09882735.acgn 1 1 19 krunat\_03012003\_073943\_15223 -NPU=6 -ICPU=3  
NO XIPXY NO MMAP LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMPOUT=120  
WARN TIMEOUT=30 -THRPAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPCP=6 -FGAPEXT=7  
YGAPOP 10 YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL\_21:  
1: sp archaea:  
2: sp bacteria:  
3: sp fungi:  
4: sp human:  
5: sp invertebrate:  
6: sp mammal:  
7: sp mbc:  
8: sp organelle:  
9: sp phage:  
10: sp plant:  
11: sp rodent:  
12: sp virus:  
13: sp vertebrate:  
14: sp unclassified:  
15: sp rvirus:  
16: sp bacteriaph:  
17: sp archaea:

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740	82.9	446	6 Q95ND3	Q95nd3 felis silve

ID	Q95ND3	PRELIMINARY	PRT	446 AA
AC	Q95ND3			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Tumor necrosis factor type 1.			
GN	TNFR I.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia, Felidae; Felis.			
OX	NCBI_TaxID=9685;			
RN	[1]			
RP	SEQUENCE FROM N A			
PA	Mizuno T., Goto Y., Raba K., Masuda K., Ohno K., Tsujimoto H.;			
PT	"Molecular cloning of feline tumor necrosis factor receptor type 1			
RT	(TNFR I) and expression of TNFR I and TNFR II in various disease in			
RT	cats."			
RL	Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB051103; BAB55455.1; -			
DR	InterPro; IPR000345; CytC_heme_bind.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR000561; EGF-like.			
DR	InterPro; IPR003368; TNFR_C6.			

## ALIGNMENTS

RESULT 1

Q95ND3 ID Q95ND3 PRELIMINARY PRT 446 AA.

AC Q95ND3

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Tumor necrosis factor type 1.

GN TNFR I.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia, Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N A

PA Mizuno T., Goto Y., Raba K., Masuda K., Ohno K., Tsujimoto H.;

PT "Molecular cloning of feline tumor necrosis factor receptor type 1

(TNFR I) and expression of TNFR I and TNFR II in various disease in

cats."

RL Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB051103; BAB55455.1; -

DR InterPro; IPR000345; CytC\_heme\_bind.

DR InterPro; IPR000488; Death.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR003368; TNFR\_C6.



DR EMBL; U72144; AAB95089.1; -;  
 DR HSSP; P19438; LEXT;  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
 KW Receptor.  
 FT NON TER 189 189  
 SQ SEQUENCE 189 AA; 21420 MW; F3FB0CE809D7DBE CRC64;  
 Alignment Scores:  
 Pred. No.: 1,95e-66 Length: 189  
 Score: 731.00 Matches: 124  
 Percent Similarity: 91.03% Conservative: 8  
 Best Local Similarity: 85.52% Mismatches: 13  
 Query Match: 77.68% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-882-735-1 (1-483) x Q95185 (1-189)  
 QY 10 TTTCTCTTAAATATATATACACCTCAAAATATTCGATTCTCTACCAAGTCCAC 69  
 DB 44 CysProGlnGlyLysTrpHisProGlnAspAsnSerIleCysCysThrLysCysHis 63  
 QY 70 AAGGAACCTACTTGACAAATGACTGTCCAGCGCGCGGAGGATACCGACTCGAGCGAG 129  
 DB 64 LysGlyThrTyLeuTyLeuAspCysGluGlyProGlyLeuAspThrAspCysArgGlu 83  
 QY 110 TTTACACATGCTTCTTTACGCTTTTCAGAAACCACTTCAGACACTCCCTACCTCTCC 189  
 DB 84 CysGluAsnGlyThrPheThrAlaSerGluAsnTyLeuArgGlnCysLeuSerCysSer 103  
 QY 130 AATCTCTTAAATATATATATACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 249  
 DB 104 LysCysArgLysGluMetTyLeuValGlnLeuSerProCysThrValTyArgAspThr 123  
 QY 238 TTTCTCTTAAATATATATATACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 309  
 DB 124 ValCysGlyCysArgLysAsnGlnTyArgTyTrpSerGluThrHisPheGlnCys 143  
 QY 310 TTTCAATCTCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 369  
 DB 144 LeuAsnCysSerLeuCysLeuAsnGlyThrValGlnLeuSerCysLysGluThrGlnAsn 163  
 QY 378 AATCTCTTAAATATATATATACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 429  
 DB 164 ThrValCysThrCysHisAlaGlyPhePheLeuArgGlyAsnGluCysValSerCysVal 183  
 QY 430 AACTTAAGAAAGC 444  
 DB 184 AmnCysLysLysAsn 188  
 RESULT 4  
 Q95MM1  
 ID Q95MM1 PRELIMINARY; PRT; 413 AA.  
 AC Q95MM1;  
 FT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE WSL\_1-like protein.  
 GN TNFRSF12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 PN [1]  
 RX NCBI TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 FX MEDLINE=21158184; PubMed=11261933;  
 RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,

RA Owen M.J.;  
 RT "Genomic structure, expression, and chromosome mapping of the mouse  
 RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)  
 RT gene";  
 RL Immunogenetics 53:59-63(2001).  
 DP EMBL; AF129969; AAF11256.1; -;  
 DR HSSP; F25942; ICDF.  
 DR MGD; MGI:1934667; Tnfrsf12.  
 DR InterPro; IPR000498; Death.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN 1.  
 CP PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DARARF CRC64;  
 Alignment Scores:  
 Pred. No.: 2,95e-12 Length: 413  
 Score: 203.50 Matches: 51  
 Percent Similarity: 44.87% Conservative: 19  
 Best Local Similarity: 32.69% Mismatches: 54  
 Query Match: 21.63% Indels: 32  
 DB: 11 Gaps: 7  
 US-09-882-735-1 (1-483) x Q99MM1 (1-413)  
 QY 52 TGCTGTACCAAGTGCATATAAAGAAATATATTTTATAATATAATATAATATAATATAAT 111  
 DB 54 CysCysArgGlyCysProLysGlyHisTyrMetLysAlaProCysAlaLubProGlyHis 74  
 QY 112 GATACCACTGTAAT 171  
 DB 74 AsnSerThrCysLeuProCysProSerAspThrPheLeuThrArgAspAsnHisHis 94  
 QY 172 CAATCTCTTAAAT 238  
 DB 94 ThrAspCysThrArgCysGlnValCysAspGluGluAlaLeuGlnValThrLeuGluAsn 114  
 QY 229 TGCACATGACACCGCGACACACCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 288  
 DB 114 CysSerAlaLysSerAspThrHisCysGlyCysGlnSerGly 128  
 QY 289 AGTCAAACCTTTCTCAGTCTTCAATTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 347  
 DB 129 CysValAspCysSerThrValProCysGlyLysSerGly 147  
 QY 338 CCGTGCCT 398  
 DB 142 oPheSerCysValProCysGlyAlaThrThrProValHisGluAlaProThrPro Arg 161  
 QY 379 ACCTGCATGACAGTTCTTTCTTAAAGAAAGACAGCTGTCTCTCTCTCTCTCTCTCT 429  
 DB 162 ProCysLeuProGlyPheTyrlleArgGlyAsnAspCysThrSerCysProThrGlyPhe 181  
 QY 427 AGTAACGTGAAGAAAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 465  
 DB 182 SerSerValCysProLysAla CysThrAlaValCys 193  
 RESULT 5  
 Q9PVD4  
 ID Q9PVD4 PRELIMINARY; PRT; 387 AA.  
 AC Q9PVD4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE p75-like transmembrane protein fullback.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Q9PUS0;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Decoy TNF receptor.  
 OS Salvelinus fontinalis (Brook trout) (Brook char).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
 OX NCBI\_TaxID=8038;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20111091; PubMed=10642582;  
 RA Robe J., Goetz F.W.;  
 RT "A tumor necrosis factor decoy receptor homologue is up-regulated in  
 RT the brook trout (Salvelinus fontinalis) ovary at the completion of  
 RT ovulation."  
 RL Biol. Reprod. 62:420-426(2000)  
 DR EMBL; AF156738; AAD56428.1; -  
 DR HSSP; O14763; IDAV.  
 DR InterPro; IPR000561; EGF-like  
 DR InterPro; IPR001368; TNFR\_C6  
 DR Pfam; PF00020; TNFR\_C6; 4  
 DR SMART; SM00208; TNFR\_4  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 1  
 KW Receptor.  
 SQ SEQUENCE 302 AA; 34017 MW; E44C73477F05C3DF CRC64;  
 Alignment Scores:  
 Pred. No.: 1,11e-10 Length: 302  
 Score: 188.00 Matches: 45  
 Percent Similarity: 46.15% Conservative: 21  
 Best Local Similarity: 31.47% Mismatches: 53  
 Query Match: 19.98% Indels: 24  
 DB: 13 Gaps: 7  
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 QY 46 TCGATTCTCTTCACTAAATGTCACAAAGTAACTACTTGTACATGACTGTCCAGGCGCG 105  
 Db 33 SerIleValCysAspArgCysProGlyThrTyrLeuArgAlaProCysSerAlaMet 52  
 QY 106 GAGACATAGCAAGTATTCAGAGAGTGTGTGAGAGGAGTCTCTTACCGGTTCCAGAAACAC 165  
 Db 53 AtqLysSerAspCysAlaValCysProAsnGlyAlaTyrThrGluPheTrpAsnHis 71  
 QY 166 CTCAGACATGCTGCTAGCTGCTCCAAATGCGCAAGGAAATGCGTCCAGGTGGAGATCTCT 225  
 Db 72 IleSerLysCysLeuArgCysSerMetCysAlaGlu-----AsnGlnValValLysGln 89  
 QY 226 TTTTTCACACTGCAACGGTACACCGTGTGTGCTGTGCTGACAGAGAACACAGTACCGGCTATT 285  
 Db 90 GluCysSerProSerAspAsnSerCysGluCysGluCysLysGluGly-----TyrTyr 106  
 QY 286 TCAAGTAAACATTTTCATGATGATTCATTAATTCAGCCCTCTCC----- 327  
 Db 107 PheAsnLysLysTyrGluAlaCysIleLysHisLysGluCysProGlyTyrGlyAla 126  
 QY 328 --CTTAATGCAATCTATATCTTCTCCAGGAGAACACAGTGTGCACCC--- 381  
 Db 127 AsnThrThrGlyThrProHis-----GlnAspThrGluCysValGln 140  
 QY 382 TGCATGCAAGTCTTTTCTTCTAGAGAAACACAG-----TGTGTCCTCTGTAGT 429  
 Db 141 CysGlnAlaGlyPheTyrSerGluValSerSerAlaLysAlaThrCysLeuAlaGlnSer 160  
 QY 430 AACTGTAG 438  
 Db 161 AsnCysLys 163  
 RESULT 8

Q9DGH7  
 ID Q9DGH7 PRELIMINARY; PRT; 285 AA.  
 AC Q9DGH7;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Fas ligand receptor soluble form (Fragment).  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bridgman J.T., Johnson A.L.;  
 RT "Fas Expression and Regulation in Hen Granulosa Cells";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDRJ databases.  
 DR EMBL; AF346475; AAG32243.1; -  
 DR HSSP; O14763; IDAV.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00531; death\_1; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 2  
 DR SMART; SM00005; DEATH\_1;  
 DR SMART; SM00008; TNFR\_2;  
 DR PROSITE; PS00117; DEATH\_DOMAIN; 1  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 285 AA; 32431 MW; A9761960CDD79E6D CRC64;  
 Alignment Scores:  
 Pred. No.: 4.04e-10 Length: 285  
 Score: 182.50 Matches: 36  
 Percent Similarity: 46.36% Conservative: 14  
 Best Local Similarity: 32.73% Mismatches: 54  
 Query Match: 19.39% Indels: 5  
 DB: 13 Gaps: 3  
 US-09-882-735-1 (1-483) X Q9DGH7 (1-285)  
 QY 52 TCGTGTACAAAGTCCCAAGAGAAAGAACTATTGTATTAATGACTGTTCAGGTTCGAGAG 111  
 Db 6 CysCysThrLysCysLysArgGlyHisValLysSerIleAspCysProLysThrGlnIle 26  
 QY 112 GATACG3ACTGACG3AGTGTGTGAGAGAGAGG---TCTCTCACGCTTCAGAAAACATCT 166  
 Db 26 -----HisCysValProCysLysCysGlyGluGluTyrMetAspHisIleAsnAspLeu 43  
 QY 169 AGACACTGCTCCAGCTGCTCCAAATGCGCAAGGAAATGCGTTCAGGTGAGATCTCTT 228  
 Db 44 AspGluCysMetArgCysArgSerCysAspLysAlaLeuGlyLeuGluValValLysAsn 63  
 QY 229 TGCACATGGGACCGGACACGCTGTGTGTGAGAGAGAAACAGTACGATATCTT 288  
 Db 64 CysThrSerThrGluAsnAlaGluCysSerCysAlaLysAsnHisTyrCysAsn 81  
 QY 289 AGTGAACAACTTTTCCAGCTGCTCAATTCAGCTGCTTCTTCAATGAGACCTGTACATC 349  
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 QY 349 TCTGCGCAGGAGAAACAGAACACCGCTTTC 378  
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 ID Q9DF34 PRELIMINARY; PRT; 357 AA.  
 AC Q9DF34;  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)



Best Local Similarity: 27.81% Mismatches: 62  
Query Match: 19.76% Indels: 25  
DR: 12 Gaps: 6

US 09-882-735-1 (1-483) x 057079 (1-320)

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QY 100 GACGCGGCGGACGATACGACATGACGAGAGTGTGACAGCGCTCTTCACCGCTTCAGAA 159  
DB 57 AsnThrThrSerAsnThrLysCysAspLysCysProAspGlyThrPheThrSerIlePro 76  
QY 160 AATCAATGAT 216  
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QY 217 GACATGCTTCTTCTGAT 276  
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DB 115 CysGluPheGluGlySerAsn-----GlyCysArgGlyCysValProSerGln 129  
QY 337 ACGTGCACCTCTCTGCGAGGAGAAACAGAACACCGTGTGCACCTGCCATGCGAGTTTC 396  
DB 130 Thr-----LysCysAspSerGlyTyr 136  
QY 397 TTCTTA-----AGAGAAAGAAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 447  
DB 137 GlyValTyrGlyTyrSerSerLysGlyAspValIleCysLysLysCysProGlyAsnIle 156  
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DB 157 AspLysCysAspLeuSerPheAsnSerIleAsp 167

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AC Q62327;  
DT 01 NOV-1996 (TREMBLrel. 01, Created)  
DT 01 NOV-1996 (TREMBLrel. 01, Last sequence update)  
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GN TNFRSF1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID:10090;  
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RP SEQUENCE FROM N.A.  
RC STRAIN:MO;  
RA Powell E.E., Wicker L.S., Peterson L.R., Todd J.A.;  
RT "Amino acid variation in the tumor necrosis factor receptor 2 is  
linked to autoimmune diabetes in NOD mice.";  
RL Genomics 0:0-0(0).  
FN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN:MO;  
RX MEDLINE-95178848; PubMed-7873884;  
RA Powell E.E., Wicker L.S., Peterson L.R., Todd J.A.;  
RT "Allelic variation of the type 2 tumor necrosis factor receptor  
gene.";  
RL Mamm Genome 5:724-727(1994)  
DR EMBL; X76401; CAA53981.1; ..  
DR HSP; P19438; INCF  
DR MGI; MGI:1314883; Tnfrsf1b.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
KW Receptor.  
FT NON\_TER 1 87 S -> T.  
FT VARIANT 87 93 T -> I.  
FT VARIANT 93 268 F -> I.  
FT VARIANT 268 345 S -> F.  
FT VARIANT 345 421 Y -> C.  
FT VARIANT 421 486  
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US 09-882-735-1 (1-483) x Q62327 (1-459)

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QY 130 TGTGAG 180  
DB 64 CysGluAlaSerMetTyrThrGlnValTyrAsnGlnIlePheArgThrCysLeuSerCysSer 83  
QY 187 TCCAAATGCCAAGGAAAT 246  
DB 84 SerSerCysSerThrAsp-----GlnValGluThrArgAlaCysThrLysGlnIleAsn 101  
QY 247 ACGTGTGTGCTGTGAGGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 294  
DB 102 ArgValCysAlaCysGluAlaGlyArgTyrCysAlaLeuLysThrHis SerGly 119  
QY 295 AACCTTTTCCAGTGTCTTCAATTCAGCGCTGCTGCTCAATGCG-----ACGCTGACCTGTC 361  
DB 120 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyValAlaSerSer 146  
QY 362 TGTCCAGGAGAAACAGAACAG 438  
DB 140 ArgAlaProAsnGlyAsnValLeuCysLysAlaCysAlaProGlyThrPhe Ser 167  
QY 409 AACGAGTGTGTCTGCTGT 468  
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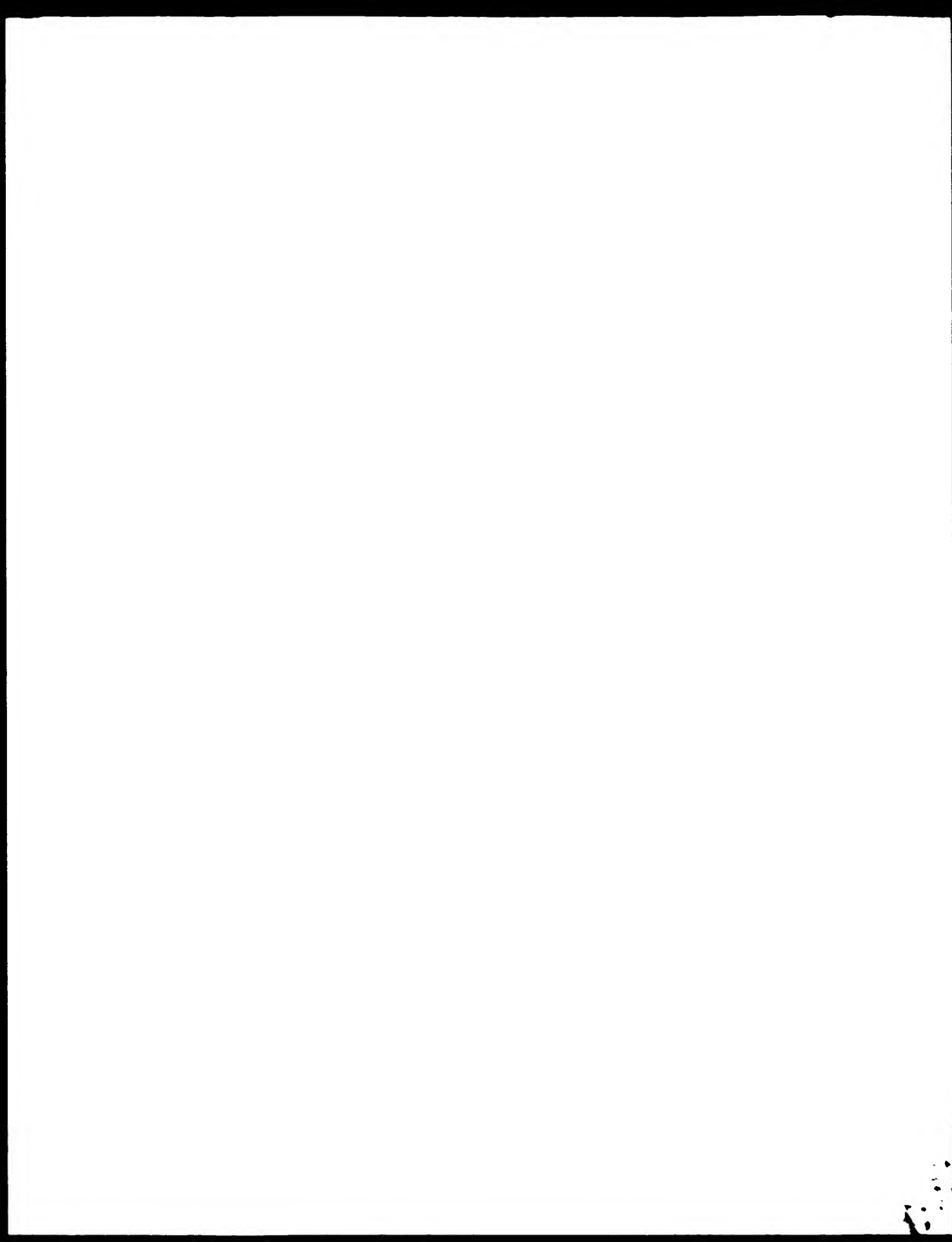
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DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
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GN FAS.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID:9031;  
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RA Bridgham J.T., Johnson A.L.;









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DB 585 CGGATACAGCTTGTGTGAGTGGAGAGAAAGTACCGGATTATTAGTGGAGAAACCTT 644  
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DB 825 AAT 827  
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DEFINITION: Sequence 7 from patent US 6194177.  
ACCESSION AR134762  
VERSION AR134762.1 GI:14123667  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1301)  
AUTHORS Campbell, P. K., Jameson, B. A. and Chappell, S. C.  
TITLE DNA encoding a hybrid heterodimeric protein  
JOURNAL Patent: US 6194177 A 7 27-FEB-2001;  
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DB 405 AAGTGGCAAAAGTAACTTGTATGATGCTTCCAGGAGCGGGGAGGATACCGGAC 464  
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DB 825 AAT 827  
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DEFINITION: H.sapiens mRNA for TNF-binding polypeptide from patent EP0391438.  
ACCESSION A29103  
VERSION A29103.1 GI:1247517  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1331)  
AUTHORS Hauptmann, R., Himmler, A., Maurer-Foy, I. and Stratowa, C.  
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
JOURNAL Patent: EP 0391438-A 53 24-OCT-1990;  
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CY 481 AAT 483  
 DB 755 AAT 757  
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 VERSION M33294.1 GI:339744  
 KEYWORDS cell surface receptor; tumor necrosis factor receptor.  
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 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 Schall T J, Lewis M, Koller K J, Lee A L, Rice G C, Wong G H,  
 Gearing D, Springer A, Luster R, Radd H, Kohli M J, and  
 Geisler R  
 Molecular cloning and expression of a receptor for human tumor  
 necrosis factor  
 Cell 61:1369-1376 (1990)  
 JOURNAL MEDLINE 90235285  
 PUBMED 2159969  
 COMMENT Direct entry and computer readable sequence for (1) kindly submitted  
 by T.Schall, 26-MAR-1990.  
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 REFERENCE 1  
 AUTHORS Niimura, K., Wagsama, M., Kanda, K., Kondo, H., Yokoi, T.,  
 Kodaira, H., Furuta, T., Takahashi, M., Kikawa, E., Omita, Y.,  
 Kashiwagi, K., Katsuta, N., Sato, K., Takikawa, Y., Imaizumi, M.,  
 Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,  
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 Nagahara, K., Masuno, Y., Nagai, K. and Isegaki, T.  
 NEDO human cDNA sequencing project  
 TITLE Unpublished  
 JOURNAL 2 (bases 1 to 2109)  
 REFERENCE Isegaki, T., Otsuki, T. and Sugiyama, T.  
 AUTHORS Direct Submission  
 COMMENT Submitted (24-OCT-2001) Takao Isegaki, Helix Research Institute,  
 Genomics Laboratory, 153-3 Yana, Kisarazu, Chiba 291-0312, Japan  
 (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-02-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
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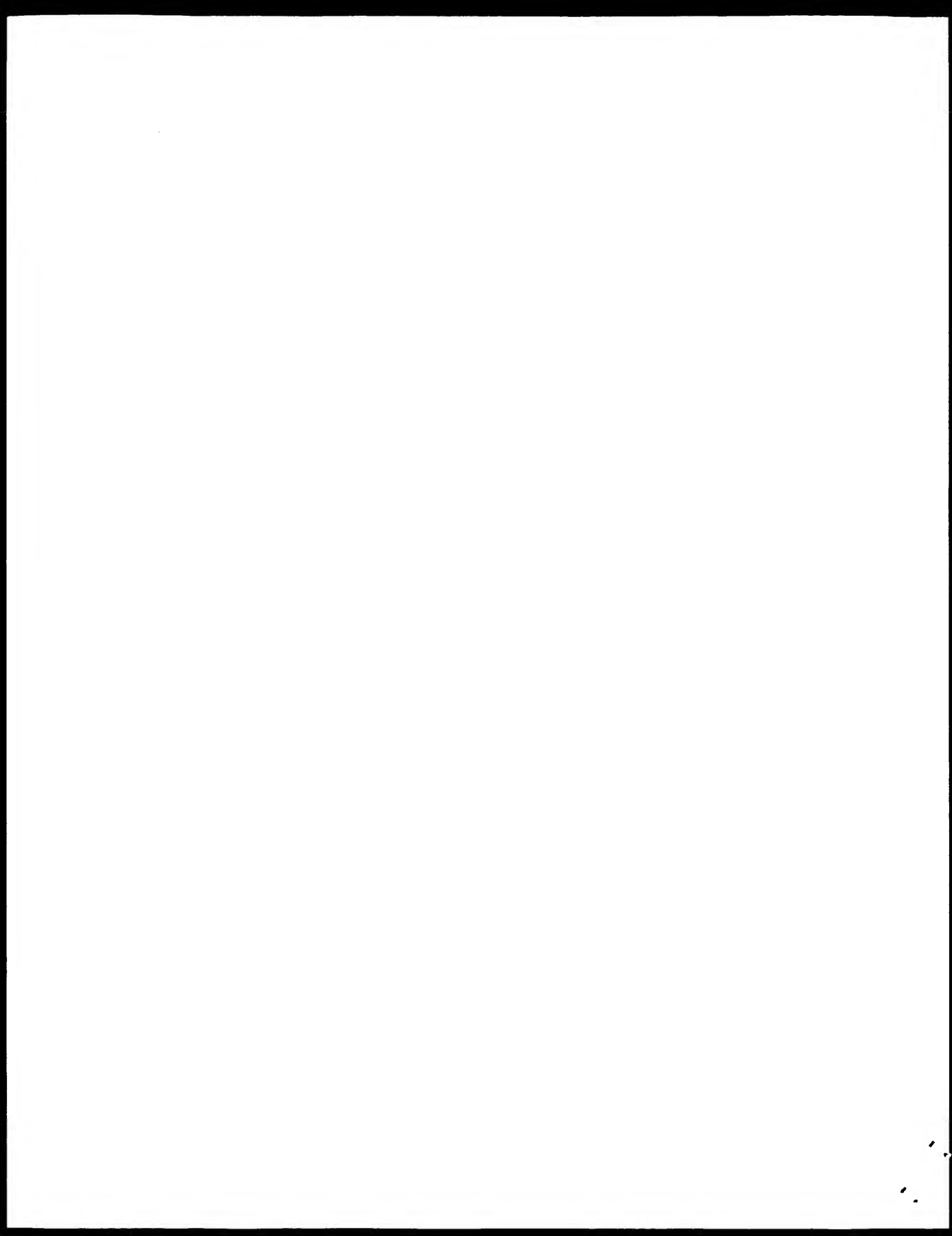




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DB 481 AAT 483
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GenCore version 5.1.3  
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Run on: January 5, 2003, 22:50:57 ; Search time 263 Seconds  
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Title: US-09-882-735-1

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Searched: 2185219 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post processing: Minimum Match 0%

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18: /SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	483	100.0	483	19	AAV41548	Human soluble tumo
2	483	100.0	483	19	AAV19801	Soluble tumour nec
3	483	100.0	483	20	AAV81732	Tumour necrosis in
4	483	100.0	483	22	AAC83945	Human 30 kDa TNF i
5	483	100.0	1301	18	AAT94032	cDNA for TBP(20-19
6	483	100.0	1334	11	AAQ66282	Plasmodium Tumour Nec
7	483	100.0	1364	21	AAQ49932	Lambda-derived TNF
8	483	100.0	1368	21	AAA95105	Human TNF1 coding
9	483	100.0	1478	20	AAV58150	CadC-fusion polype

10	483	100.0	2062	13	AAQ20973	TNF alpha binding
11	483	100.0	2062	13	AAQ24440	Encodes TNF alpha
12	483	100.0	2088	12	AAQ10883	30kD TNF inhibitor
13	483	100.0	2088	22	AAC83946	Human 30 kDa TNF i
14	483	100.0	2111	12	AAQ10955	Encodes human 30kD
15	483	100.0	2111	20	AAZ09170	Human tumour necro
16	483	100.0	2111	22	AAH48859	Human TNFEP associ
17	483	100.0	2111	24	ARF84039	Human cDNA differe
18	483	100.0	2111	24	ABH95822	Gene #246 used to
19	483	100.0	2161	21	AZ48475	Human tumour necro
20	483	100.0	2161	24	ABK13194	Human tumour necro
21	483	100.0	2175	16	AAQ90513	p55 TNF Receptor
22	483	100.0	6889	17	AAT15931	DiBP/Intein (WTAS
23	483	100.0	6926	18	AAV04431	Vector pcDNA3.1(+)
24	481.4	99.7	2141	11	AAQ06285	Human Tumour Necro
25	481.4	99.7	2176	12	AAQ12215	Type 1 TNF receptor
26	479.8	99.3	2170	14	AAQ50870	Encodes truncated
27	478.4	99.0	608	13	AAQ24441	Encodes truncated
28	475	98.3	1147	18	AAT94021	cDNA for TBP(20-19
29	424.4	87.9	1049	18	AAT94007	cDNA for TBP(20-19
30	424.4	87.9	1202	18	AAT94008	cDNA for TBP(20-19
31	415	85.9	1674	21	AAZ50196	MALE fusion plasmi
32	383	79.3	504	13	AAQ24445	Encodes truncated
33	370.8	78.2	1077	24	ABA99913	TNF selectokine p
34	357.2	74.0	474	13	AAQ24442	Encodes truncated
35	330	68.3	507	24	ABL99490	Target vaccine gene
36	312.2	64.6	339	19	AAV19804	Truncated sTNF, s
37	308	63.8	333	19	AAV19805	Truncated sTNF, s
38	304.2	63.0	332	19	AAV19803	Truncated sTNF, s
39	303.8	62.9	2130	24	APF63694	Rat sequence diff
40	299.2	61.9	5870	21	AAV15044	Nucleotide sequen
41	287.4	61.6	2173	11	AAQ66284	Rat Tumour Necrosi
42	284.6	61.0	315	19	AAV19806	Truncated sTNF, s
43	273.8	56.7	294	19	AAV19808	Truncated sTNF, s
44	264.6	54.8	285	19	AAV19807	Truncated sTNF, s
45	258	53.4	1497	21	AAZ50194	MALE fusion plasmi

#### ALIGNMENTS

##### RESULT 1

AAV41548  
ID AAV41548 standard; cDNA; 483 BP.

XX AC AAV41548;  
XX

XX DT 28-SEP-1998 (first entry)

XX DE Human soluble tumour necrosis factor receptor type I.

XX KW Human; tumour necrosis factor, TNF; TNF receptor type I;

XX KW inflammatory disease; leukaemia; TNF binding protein;

XX KW anti inflammatory drug; methotrexates; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..483

FT FT /\*tag= a

FT FT /product= "human soluble TNF receptor type I;"

XX PN WQ9824463-A2.

XX PD 11-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22733.

XX PF 09-JUL-1997; 97US-0952023.

XX PF 06-DEC-1996; 96US-0032587.

XX PP 23-JAN-1997; 97US-0036355.

XX PP 07-FEB-1997; 97US-0039315.



QY 301 TTCCAGTGTCTTAATTAAGAGGCTCTACTCAATGAGAGGTCACCTCTCTCTGCGAGGAG 360  
 Db 301 TTCCAGTGTCTTAATTAAGAGGCTCTACTCAATTAAGAGGTCACCTCTCTCTGCGAGGAG 360  
 QY 361 AAACAGAACACCGTGTGACCTGCGATGCGAGGTTTCTTTCTTAAGAGAAACGAGTGTGTC 420  
 Db 361 AAACAGAACACCGTGTGACCTGCGATGCGAGGTTTCTTTCTTAAGAGAAACGAGTGTGTC 420  
 QY 421 TCTCTTACTTAATTTAAAGAAAGGCTGGAGTGACGAGGTTGTGCTACCCGCAATTGAG 480  
 Db 421 TCTCTTACTTAATTTAAAGAAAGGCTGGAGTGACGAGGTTGTGCTACCCGCAATTGAG 480  
 QY 481 AAT 483  
 Db 481 AAT 483  
 RESULT 4  
 ID AAVR1742 standard; cDNA; 483 BP.  
 XX AC  
 XX AAVR1742;  
 DT 04 MAR 1999 (first entry)  
 XX Tumour necrosis inhibitor 30 kDa encoding cDNA.  
 DE  
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis; ss.  
 XX  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FT CDS 1..483  
 FT /\*tag= a  
 FT /note= "no stop codon given"  
 XX  
 PN WO9849405-A1.  
 XX C5-NOV-1998.  
 XX 29 APR 1998; 98WO-US08631.  
 XX 01 MAY-1997; 97US 0850188.  
 XX (AMGE-) AMGEN INC.  
 PA Boyle WJ, Wooden S;  
 PI  
 XX WPI; 1999-034661/03.  
 DR P PSDB; AAW89233.  
 XX  
 XX New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Disclosure; Fig 2; 92pp; English.  
 XX  
 CC The present invention describes a chimeric polypeptide (Al), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated Al monomers; (2) an isolated nucleic  
 CC acid encoding Al; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and

CC ligands. The present sequence encodes the TNF inhibitor 30 kDa protein.  
 XX  
 SQ Sequence 483 BP; 130 A; 124 C; 123 G; 100 T; 0 other;  
 Query Match 100.0%; Score 483; DB 20; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 9,4e-141;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 1 GATAGTGTGTCTCTCAAGGAAAAATATATCAAGCTCAAAATTAATTCATTTTAAAT 60  
 Db 1 GATAGTGTGTCTCTCAAGGAAAAATATATCAAGCTCAAAATTAATTCATTTTAAAT 60  
 QY 61 AAGTCCCAAAAGGAACCTACTTGTACAATTAATTAATTAATTAATTAATTAATTAAT 120  
 Db 61 AAGTCCCAAAAGGAACCTACTTGTACAATTAATTAATTAATTAATTAATTAATTAAT 120  
 QY 121 TGCAGGAGTGTGAGAGCGGTCTCTTCAAGGTTTCAAAAAAACAATCAAAACAATCAAA 180  
 Db 121 TGCAGGAGTGTGAGAGCGGTCTCTTCAAGGTTTCAAAAAAACAATCAAAACAATCAAA 180  
 QY 181 AGCTGCTCCAAATGCGGAAAGAAATGCTGAGTGAATATCTCTCTCTCTCTCTCTCT 240  
 Db 181 AGCTGCTCCAAATGCGGAAAGAAATGCTGAGTGAATATCTCTCTCTCTCTCTCTCT 240  
 QY 241 CGGAGACACCGT 300  
 Db 241 CGGAGACACCGT 300  
 QY 301 TTCCAGTGTCTTAATTAAGAGGCTCTACTCAATGAGAGGTCACCTCTCTCTGCGAGG 360  
 Db 301 TTCCAGTGTCTTAATTAAGAGGCTCTACTCAATGAGAGGTCACCTCTCTCTGCGAGG 360  
 QY 361 AAACAGAACACCGTGTGACCTGCGATGCGAGGTTTCTTTCTTAAGAGAAACGAGTGTG 420  
 Db 361 AAACAGAACACCGTGTGACCTGCGATGCGAGGTTTCTTTCTTAAGAGAAACGAGTGTG 420  
 QY 421 TCTCTTACTTAATTTAAAGAAAGGCTGGAGTGACGAGGTTGTGCTACCCGCAATTGAG 480  
 Db 421 TCTCTTACTTAATTTAAAGAAAGGCTGGAGTGACGAGGTTGTGCTACCCGCAATTGAG 480  
 QY 481 AAT 483  
 Db 481 AAT 483  
 RESULT 4  
 AAC83945  
 ID AAC83945 standard; DNA; 483 BP.  
 XX  
 XX AAC83945;  
 DT 02-MAR-2001 (first entry)  
 XX Human 30 kDa TNF inhibitor coding sequence #1.  
 DE  
 XX TNF inhibitor; antinflammatory; Tumour Necrosis Factor; interleukin;  
 KW IL-1; inflammatory disease; degenerative disease; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6143866-A.  
 XX  
 PD 07-NOV-2000.  
 XX  
 PF 19-JAN-1995; 95US-0375242.  
 XX  
 PR 19-JUL-1990; 90US-0555274.  
 PR 09-JUL-1993; 93US-0090366.  
 PR 18-JUL-1989; 89US-0381080.  
 PR 11 DEC-1989; 89US 0450329.  
 PR 07-FEB-1990; 90US-0479661.  
 XX  
 PA (AMGE-) AMGEN INC.









XX (GENA) GENAISSANCE PHARM INC.  
 PA (NAND/) NANDABALAN K.  
 PA (SCHU/) SCHULZ V P.  
 PA (STEP/) STEPHENS J C.  
 PA (CHEW/) CHEW A.  
 XX  
 PI Nandabalan K, Schulz VP, Stephens JC, Chew A;  
 XX  
 XX WPI: 2000-543909/49.  
 DR P-PSDB; AAR21446.  
 XX  
 XX Polynucleotides comprising polymorphic variants of a reference sequence  
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the  
 PT biological function of TNFR1 and identifying drugs targeting the  
 PT protein for treating disorders -  
 XX  
 PS "Claim 7; Fig 4; 79pp; English.  
 XX  
 CC The present invention relates to polymorphic variants of the tumour  
 CC necrosis factor receptor 1 (TNFR1) gene. The present sequence is  
 CC the coding sequence of the TNFR1 gene. The sequence of the whole gene is  
 CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were  
 CC identified by amplifying and sequencing regions of the gene. Twelve  
 CC polymorphic loci were discovered. Of these twelve polymorphisms, four can  
 CC cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be  
 CC useful for studying the biological function of TNFR1 as well as for  
 CC identifying drugs targeting the protein for treatment of disorders  
 CC related to its abnormal expression or function such as tumours,  
 CC apoptosis related disorders and bacterial infection.  
 XX  
 XX Sequence 1368 BP; 202 A; 424 C; 376 G; 276 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 483; DB 21; Length 1368;  
 Best Local Similarity 100.0%; Pred No. 1.5e-140;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0,  
 QY 1 GATAGTGTGTGTCGCGCAAGCAAAATATATATGACCGCTGAAATATATGATTTGTGTACC 60  
 DB 121 GATAGTGTGTGTCGCGCAAGCAAAATATATATGACCGCTGAAATATATGATTTGTGTACC 180  
 QY 61 AAGTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 120  
 DB 181 AAGTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 240  
 QY 121 TGACGAGAGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 180  
 DB 241 TGACGAGAGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 300  
 QY 181 AGCTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 240  
 DB 301 AGCTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 360  
 QY 241 GCGGACACCGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 300  
 DB 361 GCGGACACCGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 420  
 QY 301 TTTCAGTGTGTTCAATGTGACGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 360  
 DB 421 TTTCAGTGTGTTCAATGTGACGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 480  
 QY 361 AAACAGACACCGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 420  
 DB 481 AAACAGACACCGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 540  
 QY 421 TCTGTGTAGTACGTGTAAGCAAAAGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 480  
 DB 541 TCTGTGTAGTACGTGTAAGCAAAAGCTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 600  
 QY 481 AAT 483  
 DB 601 AAT 603

RESULT 9  
 AAX58150  
 ID AAX58150 standard; DNA; 1478 BP.  
 XX  
 AC AAX58150;  
 XX  
 DT 21-JUL-1999 (first entry)  
 XX  
 DE CadC-fusion polypeptide coding sequence.  
 XX  
 KW CadC; fusion protein; tumour necrosis factor alpha interaction domain;  
 KW protein-protein interaction; periplasmic domain; transmembrane domain;  
 KW CadC transcriptional regulatory domain; receptor interaction;  
 KW ligand identification; orphan receptor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9923116-A1.  
 XX  
 PD 14-MAY-1999.  
 XX  
 PF 03-NOV-1998; 98WO-US23307.  
 XX  
 PR 09-SEP-1998; 98US-0149922.  
 PR 03-NOV-1997; 97US-0064058.  
 XX  
 PA (SMAL-) SMALL MOLECULE THERAPEUTICS INC.  
 XX  
 PI Hsing W, Menzel R, Taggart PA;  
 XX  
 DR WPI: 1999-313305/26.  
 XX  
 PT New CadC-fusion polypeptide nucleic acid constructs  
 XX  
 PS Claim 4, Fig 3a, 123pp, English.  
 XX  
 CC This sequence encodes a CadC-fusion polypeptide containing the  
 CC tumour necrosis factor alpha interaction domain.  
 CC The invention relates to CadC-fusion polypeptide nucleic acid constructs,  
 CC which are used to transform cells to produce systems for identifying  
 CC compounds which modulate interactions between protein sequences. The  
 CC CadC-fusion polypeptides comprise a periplasmic domain, a transmembrane  
 CC domain and a CadC transcriptional regulatory domain. Cells transformed  
 CC with nucleic acid encoding the fusion proteins and a cadBA reporter  
 CC construct can be used for identifying compounds which modulate a specific  
 CC protein-protein interaction such as modulation of interactions between  
 CC protein sequences involved in receptor interactions, e.g. dimerisation.  
 CC Such methods can be used for identifying ligands for orphan receptors.  
 CC The system is extremely sensitive in that background is low and the  
 CC magnitude of signal background is quite robust, such that even minor  
 CC modulations in protein-protein interactions are readily detectable.  
 XX  
 SQ Sequence 1478 BP; 398 A; 351 C; 346 G; 381 T; 2 other;  
 Query Match 100.0%; Score 483; DB 20; Length 1478;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-140;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0,  
 QY 1 GATAGTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 60  
 DB 941 GATAGTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 1000  
 QY 61 AAGTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 120  
 DB 1001 AAGTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 1060  
 QY 121 TCCAGAGAGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 140  
 DB 1061 TCCAGAGAGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 1120  
 QY 181 AGCTGTGTGTCGCGCAAGCAAAATATATGACCGCTGAAATATATGATTTGTGTACC 240





[illegible]

Query	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Sequence 3088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Best Local Similarity 100.0%; Score 483; ES 22; Length 2068;	1	249	61	349	121	409	181	469	529	301	589	361	649	421	709	481	769
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1	249	61														

PT mat peptide /\*tag= a  
 FT 274..1551  
 FT /\*tag= b  
 XX /product= 55kd TNF-RP  
 PN EP417563 A.  
 XX  
 XX 20 MAR 1991.  
 XX  
 XX 31 AUG 1990; 90EP-0116707.  
 XX  
 XX 20 APR 1990; 90CH-0001347.  
 XX 12 SEP 1989; 89CH-0003319.  
 XX 08 MAR 1990; 90CH-0000746.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 XX  
 XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 XX Schlaefer E;  
 XX  
 XX WPI; 1991-081951/12.  
 XX F PSDB; AAR11082.  
 XX  
 XX Insoluble tumour necrosis factor binding proteins - and DNA  
 XX encoding them, useful in pharmaceutical prods. and for antibody  
 XX prodn.  
 XX  
 XX Claim 4; Fig 1; 26pp; German.  
 XX  
 XX Partial amino acid sequences were determined for the 55 and 75kd  
 XX TNF BPs (see AAP11072-B11081) and oligonucleotide primers were  
 XX synthesised based on these partial sequences. The primers were used  
 XX to produce a cDNA fragment for use as a probe to screen a human  
 XX placental cDNA bank constructed in lambda gt11. Positive clones were  
 XX identified and sequenced. DNA constructs comprising the TNF-BP coding  
 XX sequence may also contain a fragment encoding a human Ig domain.  
 XX Recombinant constructs are used to transform cells to confer  
 XX improved TNF-binding properties.  
 XX See also AAQ10956.  
 XX  
 XX Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 483; DP 12; Length 2111;  
 XX Best Local Similarity 100.0%; Pred No 1 Re-140;  
 XX Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 1 GATATGTTGTTTCTGCTAAAGAAATATATATCCAGCTTAAATATATTCGATTGCTGTACC 60  
 DB |||||||  
 QY 61 AAGTCCGACAAAGAACTTACTTTTACAAATGACTGTTCAGGCGGCGGACGATACGGAC 120  
 DB |||||||  
 QY 162 AAGTCCGACAAAGAACTTACTTTTACAAATGACTGTTCAGGCGGCGGACGATACGGAC 426  
 DB |||||||  
 QY 121 TGCAGGAGTGTGACAGCGGCTTCTTACCGCTTCAGAAACACCGCTCAGACAGTGGCTC 180  
 DB |||||||  
 QY 427 TGCAGGAGTGTGACAGCGGCTTCTTACCGCTTCAGAAACACCGCTCAGACAGTGGCTC 486  
 DB |||||||  
 QY 181 AGCTGCTTCAAAATGCGGAGAAATGCGGTGAGGTGAGATCTCTTCTTCACAGTGGAC 240  
 DB |||||||  
 QY 487 AGCTGCTTCAAAATGCGGAGAAATGCGGTGAGGTGAGATCTCTTCTTCACAGTGGAC 546  
 DB |||||||  
 QY 241 CGGAGACAGGAGTGTGACAGCGGCTTCTTACCGCTTCAGAAACACCGCTCAGACAGTGGCTC 300  
 DB |||||||  
 QY 547 CGGAGACAGGAGTGTGACAGCGGCTTCTTACCGCTTCAGAAACACCGCTCAGACAGTGGCTC 606  
 DB |||||||  
 QY 301 TTTCACTGTTTCAATTGAGGCTTGGCTCAATGGGACCGGCGGACCTCTCTCCGACGAG 360  
 DB |||||||  
 QY 607 TTTCACTGTTTCAATTGAGGCTTGGCTCAATGGGACCGGCGGACCTCTCTCCGACGAG 666  
 DB |||||||  
 QY 361 AAACGACACAGGAGTGTGACAGCGGCTTCTTACCGCTTCAGAAACACCGCTCAGACAGTGGCTC 420  
 DB |||||||  
 QY 662 AAACGACACAGGAGTGTGACAGCGGCTTCTTACCGCTTCAGAAACACCGCTCAGACAGTGGCTC 726

QY 421 TCTGTAGTAACTGTAAAGAAAGCTGAGTGCACAGAAAGTGTGTGCTAAGAGATTGTA; 480  
 DB |||||||  
 DB 727 TCTGTAGTAACTGTAAAGAAAGCTGAGTGCACAGAAAGTGTGTGCTAAGAGATTGTA; 786  
 QY 481 AAT 483  
 DB |||||  
 DB 787 AAT 789  
 RESULT 15  
 AAZ09170  
 ID AAZ09170 standard; cDNA; 2111 BP.  
 XX  
 XX AC AAZ09170;  
 XX  
 XX 18-OCT-1999 (first entry)  
 XX  
 XX Human tumour necrosis factor binding protein cDNA.  
 XX  
 XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;  
 XX anti-inflammatory; antimalarial; treatment; septic shock; inflammation;  
 XX autoimmune glomerulonephritis; cerebral malaria; immune response;  
 XX antagonist; diagnosis; ds.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX Key Location/Qualifiers  
 XX FH CDS 187..1554  
 XX FT /\*tag= a  
 XX FT sig\_peptide /product= "TNF binding protein"  
 XX FT 187..273  
 XX FT /\*tag= b  
 XX FT mat\_peptide 274..1551  
 XX FT /\*tag= c  
 XX EP939121.A2.  
 XX  
 XX 01-SEP-1999.  
 XX  
 XX 31-AUG-1990, 90EP-0116707  
 XX  
 XX 20-APR-1990, 90CH-0001347.  
 XX 12-SEP-1989; 89CH-0003319.  
 XX 08-MAR-1990, 90CH-0000746.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE & CO AG F.  
 XX  
 XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 XX Schlaefer E;  
 XX  
 XX WPI; 1991-081951/12.  
 XX F PSDB; AAY30934.  
 XX  
 XX New insoluble proteins, and fragments, that bind to tumor necrosis  
 XX factor, used to treat e.g. septic shock or cerebral malaria  
 XX  
 XX Claim 4; Fig 1; 25pp; German.  
 XX  
 XX This invention describes novel homogeneous insoluble proteins (I),  
 XX their (insoluble) fragments (Ia) and their salts that can bind tumor  
 XX necrosis factor (TNF). The products of the invention have  
 XX anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)  
 XX to treat diseases in which TNF is involved (e.g. septic shock, autoimmune  
 XX glomerulonephritis, cerebral malaria, immune responses and inflammation).  
 XX (ii) to purify TNF. (iii) to identify TNF (antagonists and (iv) for  
 XX diagnostic determination of TNF in body fluids. Antibodies raised against  
 XX (I) are used for affinity purification of (I). This sequence encodes  
 XX a tumour necrosis factor binding protein described in the method of  
 XX the invention.  
 XX  
 XX Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;



GenCore version 5.1.3  
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CM nucleic nucleic search, using sw model

Run on: January 5, 2003, 22:52:37 : Search time 51 Seconds  
(without alignments)  
2904 409 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 483

Sequence: 1 gataatggtgtgtcccaagg gctaccacagattgagaat 483

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgm2\_6/ptodata/1/ina/5A\_COMB seq.\*
- 2: /cgm2\_6/ptodata/1/ina/5B\_COMB seq.\*
- 3: /cgm2\_6/ptodata/1/ina/6A\_COMB seq.\*
- 4: /cgm2\_6/ptodata/1/ina/6B\_COMB seq.\*
- 5: /cgm2\_6/ptodata/1/ina/PTTUS\_COMB seq.\*
- 6: /cgm2\_6/ptodata/1/ina/backfile1 seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	100.0	483	US-09-326-394-1	Sequence 1, Appli
2	483	100.0	1301	US-08-804-166-7	Sequence 7, Appli
3	483	100.0	1301	US-08-910-991-7	Sequence 7, Appli
4	483	100.0	1478	US-09-149-922-6	Sequence 6, Appli
5	483	100.0	2062	US-08-050-319B-24	Sequence 24, Appl
6	483	100.0	2062	US-08-465-982-4	Sequence 24, Appl
7	483	100.0	2161	US-09-106-038A-1	Sequence 1, Appli
8	483	100.0	2161	US-09-505-250-3	Sequence 3, Appli
9	483	100.0	2175	US-08-321-668-1	Sequence 1, Appli
10	483	100.0	2175	US-08-837-941-1	Sequence 1, Appli
11	483	100.0	2175	US-08-176-016-1	Sequence 1, Appli
12	483	100.0	2175	US-08-054-970-1	Sequence 1, Appli
13	483	100.0	6889	US-08-286-740-2	Sequence 2, Appli
14	483	100.0	6889	PTT-US95-09576-2	Sequence 2, Appli
15	483	100.0	6806	US-08-627-151A-6	Sequence 6, Appli
16	475.2	98.4	600	US-08-050-319B-47	Sequence 47, Appl
17	475.2	98.4	600	US-08-465-982-47	Sequence 47, Appl
18	475	98.3	1147	US-08-804-166-5	Sequence 5, Appli
19	475	98.3	1147	US-08-910-991-5	Sequence 5, Appli
20	424.4	87.9	1049	US-08-804-166-1	Sequence 1, Appli
21	424.4	87.9	1049	US-08-910-991-1	Sequence 1, Appli
22	424.4	87.9	1202	US-08-804-166-3	Sequence 3, Appli
23	424.4	87.9	1202	US-08-910-991-3	Sequence 3, Appli
24	383	79.3	504	US-08-050-319B-56	Sequence 56, Appl
25	383	79.3	504	US-08-465-982-56	Sequence 56, Appl
26	381	78.9	501	US-08-050-319B-1	Sequence 1, Appli
27	381	78.9	501	US-08-465-982-1	Sequence 1, Appli

Sequence 1, Appli  
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Sequence 49, Appli  
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Sequence 10, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 53, Appli  
Sequence 53, Appli  
Sequence 51, Appli  
Sequence 51, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 898, Appli  
Sequence 2607, Appli  
Sequence 1, Appli  
Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-326-394-1

; Sequence 1, Application US/09326394

; Patent No. 6306820

; GENERAL INFORMATION:

; APPLICANT: Bendele, Alison M.

; APPLICANT: Sennello, Regina M.

; APPLICANT: Edwards, Carl K.

; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 DeHavilland Drive

; CITY: Thousand Oaks

; STATE: CA

; COUNTRY: US

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/326,394

; FILING DATE: 08-DEC-1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/032,587

; FILING DATE: 06-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,355

; FILING DATE: 23-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/039,315

; FILING DATE: 07-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/052,023

; FILING DATE: 09-JUL-1997

; ATTOPREV/AGENT INFORMATION:

; NAME: Zindrick, Thomas K.

; REGISTRATION NUMBER: 32,185

; REFERENCE/DOCKET NUMBER: A-430D

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 483 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: CDNA

PRIOR APPLICATION DATA

NUMBER OF SEQUENCES: 22



CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,991  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/004,166  
 FILING DATE: 20 February 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/011,936  
 FILING DATE: 20 February 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 REFERENCE/DOCKET NUMBER: CAMPRELL-28  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737 3528  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1301 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 279..1287  
 US 08 910-991.7

Query Match 100.0%; Score 483; DB 4; Length 1301;  
 Best Local Similarity 100.0%; Pred No. 4.5e-146;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTGCTGTACC 60  
 DB 345 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTGCTGTACC 404  
 QY 61 AAGTGCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCCGGGCGAGGATACGGAC 120  
 DB 405 AAGTGCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCCGGGCGAGGATACGGAC 464  
 QY 121 TGCAGGGAGTGTGAGAGCGGTCTCTTCCAGGCGCTTCAGAAAACCACTCAGACACTGCCTC 180  
 DB 465 TGCAGGGAGTGTGAGAGCGGTCTCTTCCAGGCGCTTCAGAAAACCACTCAGACACTGCCTC 524  
 QY 181 AGCTGCTCCAAATCCGAAAGGAATGCGTCAAGTGGAGATCTCTTCTTGCACAGTGGAC 240  
 DB 525 AGCTGCTCCAAATCCGAAAGGAATGCGTCAAGTGGAGATCTCTTCTTGCACAGTGGAC 584  
 QY 241 CGGACACCGTGTGGCTGCGAGGAACCACTACCGGCATTATTGGAGTGAACCTT 300  
 DB 585 CGGACACCGTGTGGCTGCGAGGAACCACTACCGGCATTATTGGAGTGAACCTT 644  
 QY 301 TTCCAGTCTTCAATTGCGCTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 360  
 DB 645 TTCCAGTCTTCAATTGCGCTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 704  
 QY 361 AAACAGAACACCGTGTGCACTGCGCATGCAAGTTCCTTTCTTAAGAGAAAACGAGTGTGC 420  
 DB 705 AAACAGAACACCGTGTGCACTGCGCATGCAAGTTCCTTTCTTAAGAGAAAACGAGTGTGC 764

QY 421 TCCTGTAGTAACTGTAGAAAGGCTTGAATGTCAAGAAAGTGTGTCTATGTCAGATTGAG 480  
 DB 765 TCCTGTAGTAACTGTAGAAAGGCTTGAATGTCAAGAAAGTGTGTCTATGTCAGATTGAG 824  
 QY 481 AAT 483  
 DB 825 AAT 827  
 RESULT 4  
 US-09-149-922-6  
 ; Sequence 6, Application US/09/49922A  
 ; Patent No. 6265174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Menzel, Rolf  
 ; APPLICANT: Hsing, Weihong  
 ; APPLICANT: Taggart, Pamela  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING AND MODULATING  
 ; FILE REFERENCE: 9366-006  
 ; CURRENT APPLICATION NUMBER: US/09/149,922A  
 ; CURRENT FILING DATE: 1998-09-09  
 ; EARLIER APPLICATION NUMBER: 60/064,058  
 ; EARLIER FILING DATE: 1997-11-03  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1478  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: 58  
 ; OTHER INFORMATION: n=a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: 105  
 ; OTHER INFORMATION: n=a, c, g, or t  
 US-09-149-922-6

Query Match 100.0%; Score 483; DB 4; Length 1478;  
 Best Local Similarity 100.0%; Pred No. 4.8e-146;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTGCTGTACC 60  
 DB 941 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTGCTGTACC 1000  
 QY 61 AAGTGCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCCGGGCGAGGATACGGAC 120  
 DB 1001 AAGTGCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCGCCGGGCGAGGATACGGAC 1060  
 QY 121 TGCAGGGAGTGTGAGAGCGGTCTCTTCCAGGCGCTTCAGAAAACCACTCAGACACTGCCTC 180  
 DB 1061 TGCAGGGAGTGTGAGAGCGGTCTCTTCCAGGCGCTTCAGAAAACCACTCAGACACTGCCTC 1120  
 QY 181 AGCTGCTCCAAATCCGAAAGGAATGCGTCAAGTGGAGATCTCTTCTTGCACAGTGGAC 240  
 DB 1121 AGCTGCTCCAAATCCGAAAGGAATGCGTCAAGTGGAGATCTCTTCTTGCACAGTGGAC 1180  
 QY 241 CGGACACCGTGTGGCTGCGAGGAACCACTACCGGCATTATTGGAGTGAACCTT 300  
 DB 1181 CGGACACCGTGTGGCTGCGAGGAACCACTACCGGCATTATTGGAGTGAACCTT 1240  
 QY 301 TTCCAGTCTTCAATTGCGCTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 360  
 DB 1241 TTCCAGTCTTCAATTGCGCTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 1300  
 QY 361 AAACAGAACACCGTGTGCACTGCGCATGCAAGTTCCTTTCTTAAGAGAAAACGAGTGTGC 420  
 DB 1301 AAACAGAACACCGTGTGCACTGCGCATGCAAGTTCCTTTCTTAAGAGAAAACGAGTGTGC 1460  
 QY 421 TCCTGTAGTAACTGTAGAAAGGCTTGAATGTCAAGAAAGTGTGTCTATGTCAGATTGAG 480











TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6889 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US 08 286-740 2

Query Match 100.0%; Score 483; DB 1; Length 6889;

Best Local Similarity 100.0%; Pred No 1e-145;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATAGTGTGTCTCCCAAGCAAAATATATCCACCTCAAAATATATCGATTGCTGAC 60  
DB 1725 GATAGTGTGTCTCCCAAGCAAAATATATCCACCTCAAAATATATCGATTGCTGAC 1784  
QY 61 AAGTGTCTCAAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAGTCTGAC 120  
DB 1785 AAGTGTCTCAAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAGTCTGAC 1844  
QY 121 TGCAGGAGTGTGAGAGGGGTCTCTTCAAGTCTGAGTCTGAC 180  
DB 1845 TGCAGGAGTGTGAGAGGGGTCTCTTCAAGTCTGAGTCTGAC 1904  
QY 181 AGTGTCTCAAAATCCGAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAG 240  
DB 1905 AGTGTCTCAAAATCCGAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAG 1964  
QY 241 CGGAGACACCGT 300  
DB 1965 CGGAGACACCGT 2024  
QY 301 TTCCAGTCTCAATTCGAGCTCTGCTCAATGGAGCGTGCACCTCTCTGCGCAGGAG 360  
DB 2025 TTCCAGTCTCAATTCGAGCTCTGCTCAATGGAGCGTGCACCTCTCTGCGCAGGAG 2084  
QY 361 AAACAGACACCGT 420  
DB 2085 AAACAGACACCGT 2144  
QY 421 TCTGTATTAATCTGAAGAAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
DB 2145 TCTGTATTAATCTGAAGAAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2204  
QY 481 AAT 483  
DB 2205 AAT 2207

## RESULT 14

PCT-US95-09576-2

Sequence 2, Application PC/TUS950476

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC

TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09576

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA: 08/286740

APPLICATION NUMBER: 08/286740

FILING DATE: 05-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 798PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 6889 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

PCT-US95-09576-2

Query Match 100.0%; Score 483; DB 5; Length 6889;

Best Local Similarity 100.0%; Pred No 1e-145;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATAGTGTGTCTCCCAAGCAAAATATATCCACCTCAAAATATATCGATTGCTGAC 60  
DB 1725 GATAGTGTGTCTCCCAAGCAAAATATATCCACCTCAAAATATATCGATTGCTGAC 1784  
QY 61 AAGTGTCTCAAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAGTCTGAC 120  
DB 1785 AAGTGTCTCAAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAGTCTGAC 1844  
QY 121 TGCAGGAGTGTGAGAGGGGTCTCTTCAAGTCTGAGTCTGAC 180  
DB 1845 TGCAGGAGTGTGAGAGGGGTCTCTTCAAGTCTGAGTCTGAC 1904  
QY 181 AGTGTCTCAAAATCCGAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAG 240  
DB 1905 AGTGTCTCAAAATCCGAAAGCAAACTACTTGTATCAATGATCTTCAAGTCTGAG 1964  
QY 241 CGGAGACACCGT 300  
DB 1965 CGGAGACACCGT 2024  
QY 301 TTCCAGTCTCAATTCGAGCTCTGCTCAATGGAGCGTGCACCTCTCTGCGCAGGAG 360  
DB 2025 TTCCAGTCTCAATTCGAGCTCTGCTCAATGGAGCGTGCACCTCTCTGCGCAGGAG 2084  
QY 361 AAACAGACACCGT 420  
DB 2085 AAACAGACACCGT 2144  
QY 421 TCTGTATTAATCTGAAGAAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
DB 2145 TCTGTATTAATCTGAAGAAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2204  
QY 481 AAT 483  
DB 2205 AAT 2207

## RESULT 15

US-08-627-151A-6

Sequence 6, Application US/08627151A

Patent No. 5866341

GENERAL INFORMATION:

APPLICANT: SPINFELIA, Dominic

APPLICANT: BECHERER, Kathleen

APPLICANT: BROWN, Steven

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: SCREENING DRUG LIBRARIES







	Matches	483;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	GATG	GTGTG	TGCCCCAAGAAATAATATATACACCCCTCAAAAATATATGATTTGCTGTACC	60					
Db	1	GATG	GTGTGTGTCCCAAGAAATAATATATACACCCCTCAAAAATATATGATTTGCTGTACC	60						
Oy	61	AAGTGC	CAAAAGAAACCTACTTGTACATGACTGTGTCCAGGCGCGGAGGAGATACGAGAC	120						
Db	61	AAGTGC	CAAAAGAAACCTACTTGTACATGACTGTGTCCAGGCGCGGAGGAGATACGAGAC	120						
Oy	121	TGCAGG	GAGGTGAGAGCGGCTCCTTCAACCGTTTCAGAAAAACCACTCAGACACTGTGCCTC	180						
Db	121	TGCAGG	SAAGTGTAGAGCGGCTCCTTCAACCGTTTCAGAAAAACCACTCAGACACTGTGCCTC	180						
Oy	181	AGTGTCTC	CAATATGCGGAAAGSAAATGSGTCAAGTGCAGATCTTCTTTTGACACATGGAGAC	240						
Db	181	AGTGTCTC	CAAAATGCGGAAAGSAAATGSGTCAAGTGCAGATCTTCTTTTGACACATGGAGAC	240						
Oy	241	CGGAGAC	CCGTTGTGTGGCTGCAGAGAAACAGTACCGGACTTATTTGAGTGTAAAACTTT	300						
Db	241	CGGAGAC	CCGTTGTGTGGCTGCAGAGAAACAGTACCGGACTTATTTGAGTGTAAAACTTT	300						
Oy	301	TTCCAGTGTCTT	CAATTGTGCAGCTCTTGCTCTCAATGAGACCGTGCACCTCTCTGCTCCAGAGAC	360						
Db	301	TTCCAGTGTCTT	CAATTGTGCAGCTCTTGCTCTCAATGAGACCGTGCACCTCTCTGCTCCAGAGAC	360						
Oy	361	AAACAGAA	CCGTTGTGCACCTGCACATCAAGTTCTTTCTAAGAGAGAAAACGAGTGTGTCTC	420						
Db	361	AAACAGAA	CCGTTGTGCACCTGCACATCAAGTTCTTTCTAAGAGAGAAAACGAGTGTGTCTC	420						
Oy	421	TCTCTG	TAGTAACTGTAAAGAAACCTGSAAGTGCACGAAATTTGTCTCAATCCCAAGATTGAG	480						

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RESULT 3
US-09-792-356-3
? Sequence 3, Application US/09792356
? Publication No. US20020183485A1
? GENERAL INFORMATION:
? APPLICANT: Hauptmann, Rudolph
? APPLICANT: Himmler, Adolph
? APPLICANT: Maurer-Fogy, Ingrid
? APPLICANT: Stratowa, Christian
? TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
? FILE OF INVENTION: Them
? FILE REFERENCE: 98,385-G
? CURRENT APPLICATION NUMBER: US/09/792,356
? CURRENT FILING DATE: 2001-08-17
? PRIOR APPLICATION NUMBER: 08/477,639
? PRIOR FILING DATE: 1995-06-07
? PRIOR APPLICATION NUMBER: 08/383,676
? PRIOR FILING DATE: 1995-02-01
? PRIOR APPLICATION NUMBER: 08/153,287
? PRIOR FILING DATE: 1993-11-17
? PRIOR APPLICATION NUMBER: 07/821,750
? PRIOR FILING DATE: 1992-01-02
? PRIOR APPLICATION NUMBER: 07/511,430
? PRIOR FILING DATE: 1990-04-20
? NUMBER OF SEQ ID NOS: 87
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 463
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(483)
US-09-792-356-3

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Query Match 100.0%; Score 483; DB 9; Length 483;  
Best Local Similarity 100.0%; Pred. No. 2.2e-148;  
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATGTTGTCCTCCCAAGGAAATATATATCCACCTCCAAAATAATTCGATTGCTGACC 60  
DB 1 GATATGTTGTCCTCCCAAGGAAATATATATCCACCTCCAAAATAATTCGATTGCTGACC 60

QY 61 AAGTGCACAAAGGAACTTACTTGTACATGCTCCAGGCGCCGGGCGAGGATACGGAC 120  
DB 61 AAGTGCACAAAGGAACTTACTTGTACATGCTCCAGGCGCCGGGCGAGGATACGGAC 120

QY 121 TGCAGGAGTGTGAGAGGCGCTTCTTCCAGGCGCTTCCAGGCGCGGGGCGAGGATACGGAC 180  
DB 121 TGCAGGAGTGTGAGAGGCGCTTCTTCCAGGCGCTTCCAGGCGCGGGGCGAGGATACGGAC 180

QY 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGTGAGGATGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 240  
DB 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGTGAGGATGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 240

QY 241 CGGACACCGCTGTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 300  
DB 241 CGGACACCGCTGTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 300

QY 301 TTCCAGTGTTCATTTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 360  
DB 301 TTCCAGTGTTCATTTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 360

QY 361 AAACAGAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 420  
DB 361 AAACAGAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 420

QY 421 TCTGTAGTAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 480  
DB 421 TCTGTAGTAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 480

QY 481 AAT 483  
DB 481 AAT 483

RESULT 4  
US-09-899-422-3  
Sequence 3, Application US/09899422  
Patent No. US20020090676A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fody, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98 385-H  
CURRENT APPLICATION NUMBER: US/09/899,422  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 09/183,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 483  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: CDS  
LOCATION: (1) (483)  
US-09-899-422-3

Query Match 100.0%; Score 483; DB 10; Length 483;  
Best Local Similarity 100.0%; Pred. No. 2.2e-148;  
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATGTTGTCCTCCCAAGGAAATATATATCCACCTCCAAAATAATTCGATTGCTGACC 60  
DB 1 GATATGTTGTCCTCCCAAGGAAATATATATCCACCTCCAAAATAATTCGATTGCTGACC 60

QY 61 AAGTGCACAAAGGAACTTACTTGTACATGCTCCAGGCGCGGGGCGAGGATACGGAC 120  
DB 61 AAGTGCACAAAGGAACTTACTTGTACATGCTCCAGGCGCGGGGCGAGGATACGGAC 120

QY 121 TGCAGGAGTGTGAGAGGCGCTTCTTCCAGGCGCTTCCAGGCGCGGGGCGAGGATACGGAC 180  
DB 121 TGCAGGAGTGTGAGAGGCGCTTCTTCCAGGCGCTTCCAGGCGCGGGGCGAGGATACGGAC 180

QY 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGTGAGGATGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 240  
DB 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGTGAGGATGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 240

QY 241 CGGACACCGCTGTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 300  
DB 241 CGGACACCGCTGTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 300

QY 301 TTCCAGTGTTCATTTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 360  
DB 301 TTCCAGTGTTCATTTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 360

QY 361 AAACAGAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 420  
DB 361 AAACAGAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 420

QY 421 TCTGTAGTAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 480  
DB 421 TCTGTAGTAACTGTGAGGCGCTTCTTCCAGGCGCGGGGCGAGGATACGGAC 480

QY 481 AAT 483  
DB 481 AAT 483

RESULT 5  
US-09-907-263-1  
Sequence 1, Application US/09907263  
Patent No. US20020119924A1  
GENERAL INFORMATION:  
APPLICANT: Bendelle, Alison M.  
APPLICANT: Sennello, Regina M.  
APPLICANT: Edwards, Carl K.  
TITLE OF INVENTION: PROTEIN FOR TREATING THE MEDICALLY CHALLENGING  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: US  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/907,263  
FILING DATE: 17-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:



Db 424 TCCTGTAGTAACTGTAAAGAAAGCTGTGAGTGGAGAAAGTTGTTGCTATGCTTAACTCCCAATATGCA, 481

QY 481 AAT 483  
|||

Db 484 AAT 486

RESULT 8  
US-09-899-429A-15  
; Sequence 15, Application US/09899429A  
; Patent No. US20020169118A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmeler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; TITLE OF INVENTION: Them  
; FILE REFERENCE: 98-385-J  
; CURRENT APPLICATION NUMBER: US/09/899,429A  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/792,356  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 08/477,639  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recombinant  
; OTHER INFORMATION: TNF-BP sequence  
; NAME/KEY: CDS  
; LOCATION: (1)..(519)  
US-09-899-429A-15

Query Match 100.0%; Score 483; DB 9; Length 519;  
Best Local Similarity 100.0%; Pred. No. 2,3e-148;  
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 GATAGTGTGTGTCCTCCCAAGGAAATATATATACCTTCAAAATTAATTCGATTTCGTACC 96  
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QY 61 AAGTGGCACAAGAAAGAACTATCTTGTATCAATCACTGCTCAAGTGGGAGATATCAAT 120  
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Db 97 AAGTGGCACAAGAAAGAACTATCTTGTATCAATCACTGCTCAAGTGGGAGATATCAAT 156  
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QY 121 TGCAGGAGTGTGACAGCGGTCTTTCAATGTTTAAAGAAATCACTCAGAACTTCCTC 180  
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Db 157 TGCAGGAGTGTGACAGCGGTCTTTCAATGTTTAAAGAAATCACTCAGAACTTCCTC 216  
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QY 181 AGCTGCTCAAAATGCCGAAAGAAATGGGTAGGTGAGATCTTTTTCGTAATTCGAC 240  
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Db 217 AGCTGCTCAAAATGCCGAAAGAAATGGGTAGGTGAGATCTTTTTCGTAATTCGAC 276  
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QY 241 CGGGAACACGCTGTGTGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTG 300  
|||  
Db 277 CGGGAACACGCTGTGTGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTG 336  
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QY 301 TTCAGTGTCTCAATTCGAGCGCTTGTGCTCAATGAGTGGTGTGAGTGGTGTGAGTGGT 360  
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Db	208	TTCTAGAGATGTTAGATGGTCTTTTCAATCGTTTCAGAAAAACCACTTCAGACACTGCCTC	267
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Qy	241	TGGTACACCGGTGTGTGCTGCAGGAAGAACCAAGTACCGGCATTATTGGAGTGA AAAACCTT	300
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Qy	301	TTCCAGTCTTTCAATTGCAGCCTCTGCTCTCAATGGAGACGTGCACCTCTCTCTGCCAGGAG	360
Db	388	TTCCAGTCTTTCAATTGCAAGCTCTGCTCTCAATGGAGACGTGCACCTCTCTCTGCCAGGAG	447
Qy	361	AAATAGAAACACGTGTGCACCTGCCATGACAGGTTCCTTTCTTAAGAGAAAAACGAGTGTGTC	420
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Qy	421	TCTCTACTACTCTTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAAGATTGAG	480
Db	508	TCTCTACTACTCTTAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAAGATTGAG	567
Qy	481	AAT 483	
Db	568	AAT 570	

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RESULT 11
US 09 899,429A 11
; Sequence 11, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fody, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09,899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/421,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-RP sequence
; NAME/KEY: CDS
; LOCATION: (1)..(600)
US 09-899,429A 11

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[illegible]

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RESULT 12
US-09-899-429A-13
; Sequence 13, Application US/09/099,429A
; Patent No. US20020169118A1
; General Information:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogsy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and TNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/099,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 04/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Parent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-EP sequence
; NAME/KEY: CDS
; LOCATION: (1) (603)
US-09-899-429A-13

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Mon Jan 6 08:48:16 2003

us-09-882-735-1.rnpb

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Page 10

GenCore version 5.1.3  
Copyright (c) 1991 - 2003 CompuGen Ltd.

CM nucleic acid nucleic search, using sw model

Run on: January 6, 2003, 01:15:13, Search time 2255 Seconds  
(without alignments)  
3515.694 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 483

Sequence: 1 gatagtgtgtcccaagg .....gctaccacagattgagaat 483

Scoring table: IDENTITY NUC  
Gapop 10%, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST:

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_estc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	931	14	BQ723672
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3	483	100.0	974	12	BG180101
4	482	99.8	761	9	AU131978
5	481.4	99.7	837	9	AL522989
6	480.4	99.5	1070	13	BM546826

7	471.6	97.6	994	14	BM800044
8	467.6	96.8	975	9	AL577008
9	466.2	96.5	818	13	BI821169
10	457.6	94.7	942	9	AL529836
11	450.4	93.3	969	12	BE871809
12	448.4	92.8	859	13	BI870917
13	444.4	92.0	845	9	AU125021
14	441	91.3	872	13	BI769006
15	439	90.9	859	9	AU124446
16	438.2	90.7	767	9	AU142156
17	437.2	90.5	872	14	BQ723589
18	432.4	89.5	916	13	BI757305
19	420.6	87.1	772	9	AU137990
20	419.2	86.8	936	12	BG681438
21	415.2	86.0	823	13	BI766980
22	413.4	85.6	971	12	BE876920
23	409.4	84.8	1008	14	BQ719773
24	407.6	84.4	951	14	BQ882704
25	406.8	84.2	817	9	AL155689
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29	390.4	80.8	913	14	BQ926409
30	386.4	80.0	706	9	AU124156
31	376.4	77.9	934	13	BI831497
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33	373.6	77.3	387	14	BQ335492
34	373.2	77.3	846	13	BI917624
35	370.2	76.6	802	9	AU142163
36	369.8	76.6	805	9	AU125694
37	368.8	76.4	834	9	AU126303
38	366.8	75.9	788	9	AU124519
39	365.4	75.7	491	12	BF839822
40	357.2	74.0	822	13	BI260829
41	354.6	73.4	942	12	BE869492
42	353	73.1	416	10	BE693950
43	350	72.5	761	12	BG282718
44	348	72.0	539	14	BQ345703
45	347.6	72.0	431	14	BQ326950

#### ALIGNMENTS

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DEFINITION AGENCOURT 8489850 Lupeki dorsal root ganglion Homo sapiens cDNA  
Clone IMAGE:6184295 5', mRNA sequence.

ACCESSION BQ723672

VERSION BQ723672.1 GI:21862569

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 931)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-f@mail.nih.gov](mailto:cgapbs-f@mail.nih.gov)

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM13573 row, d column, 24

High quality sequence stop: 607.

FEATURES

Location/Qualifiers

1 931





[illegible]

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LOCUS	AL522989				
DEFINITION	AL522989.1 NT N16164.1B33 Homo sapiens cDNA clone GSDDB095p14 5				
ACCESSION	AL522989	prime, mRNA sequence.			
VERSION	AL522989.1				
KEYWORDS	EST.				
SOURCE	human.				

REFERENCE  
1. (bases 1 to 817)  
AUTHORS  
Li W.B., Guider C., Jessup J. and Polyes D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Hepatology (2001)  
COMMENT  
Contact: Genoscope

genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: [segre@genoscope.cns.fr](mailto:segre@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Location/Qualifiers

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="CSDB0009XP14"
/clone_lib="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab host="DH10B"
/note="Organ: brain; Vector: pCMWSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMWSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

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BASE COUNT	199 a	231 c	229 g	177 t	1 others
ORIGIN					

Query Match	99.7%	Score 481.4	DB 9	Length 837
Best Local Similarity	99.9%	Pred. No. 2e-142		
Matches 482	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

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LOCUS	1070 bp	linear	EST 20-FEB-2002
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DEFINITION	AGENE00027 6491128 NIH_MGC_125 Homo sapiens	CDNA clone	IMAGE:5723557
ACCESSION	5', mRNA sequence.		
VERSION	BM546826		
KEYWORDS	BM546826.1	GI:18780096	
SOURCE	EST.		
ORGANISM	human.		

ORGANISM Homo sapiens, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo. 1 (bases 1 to 1070).

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbbs-remail.nih.gov](mailto:cgapbbs-remail.nih.gov)  
 Tissue Procurement: [Invitrogen](http://www.invitrogen.com)  
 CDNA Library Preparation: [Life Technologies, Inc.](http://www.life-technologies.com)  
 CDNA Library Arrayed by: [The I M A G E Consortium \(LMNL\)](http://www.lmll.gov)  
 DNA Sequencing by: [Agencourt Bioscience Corporation](http://www.agencourt-bioscience.com)  
 Clone distribution: [MSC clone distribution](http://www.msc-clone-distribution.com) information can be  
 found through the [I.M.A.G.E. Consortium/LMNL](http://www.lmll.gov) at:  
<http://image.lmll.gov>  
 Plate: [LMML2711 row 9 column: 14](http://www.lmll.gov)  
 High quality sequence start: 2  
 High quality sequence stop: 669.  
 Location/Qualifiers

FEATURES	Location/Qualifiers
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/clone_id="NH MGC_125"
/lab_host="DH10B"
/note="Organ: ovary (pool of 3), Vector: pCMV-Sport6,
Site_1: EcoRV (destroyed), Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

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BASE COUNT      241 a   311 c   293 g   224 t       1 others
ORIGIN

Query Match      99.5%; Score 480.4; DB 13; Length 1070;
Best Local Similarity 99.2%; Pred. No. 5e-142;
Matches 481; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTCGCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 60
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DB 386 AAGTCCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 445

QY 121 TCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 180
DB 446 TCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 505

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QY 241 CGGACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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QY 301 TTCCAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTC 360
DB 626 TTCCAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTC 685

QY 361 AAACAGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 686 AAACAGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 745

QY 421 TCTGTAGTAACTGTAAGAAAGCTGCGAGTGCAGAGTGTGCTTACCCAGATTTGAG 480
DB 746 TCTGTAGTAACTGTAAGAAAGCTGCGAGTGCAGAGTGTGCTTACCCAGATTTGAG 805

QY 481 AAT 483
DB 806 AAT 808

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DEFINITION 5' mRNA sequence.
ACCESSION  RM800044
VERSION     RM800044.1 GI:19116867
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-roman@nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I M A G E Consortium (ILNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: ILNL212 row: b column: 52
            High quality sequence stop: 654.
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ORIGIN

Query Match      97.6%; Score 471.6; DB 14; Length 944;
Best Local Similarity 99.2%; Pred. No. 3.1e-139;
Matches 474; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTCGCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 60
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DB 346 AAGTCCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 400

QY 121 TGCAGGAGTGTGAGAGCGGCTGCTTCAAAATATTCGATTCGTGTACC 180
DB 406 TGCAGGAGTGTGAGAGCGGCTGCTTCAAAATATTCGATTCGTGTACC 465

QY 181 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 466 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525

QY 241 CGGACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 526 CGGACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 385

QY 301 TTCAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTC 360
DB 586 TTCAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTCATTTGAGTGTTC 640

QY 361 AAACAGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 646 AAACAGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705

QY 421 TCTGTAGTAACTGTAAGAAAGCTGCGAGTGCAGAGTGTGCTTACCCAGATTTGAG 478
DB 706 TCTGTAGTAACTGTAAGAAAGCTGCGAGTGCAGAGTGTGCTTACCCAGATTTGAG 763

RESULT 8
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LOCUS      AL577008 LTI_NFL006.PL2 Homo sapiens cDNA clone CS00108.VAG1.5
DEFINITION prime, mRNA sequence.
ACCESSION  AL577008
VERSION     AL577008.1 GI:12939716
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 975)
            Li, W., Gruber, C., Jessee, J. and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
            1..975
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RESULT 10
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prime, mRNA sequence.
ACCESSION AL529816
VERSION AL529816.1
KEYWORDS GI:12793329
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
RP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/sex="male"
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/lab_host="DH10B"
/notes="Organ: brain, Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 208 a 259 c 248 g 224 t 3 others
ORIGIN
Query Match 94.7%, Score 457.6, DB 9; Length 942,
Best Local Similarity 99.2%; Pred. No. B 9e-135;
Matches 480; Conservative 1; Mismatches 2; Gaps 2;
QY 1 GATAGTGTGTGTCGCCAAGGAAAATATATCCACCCCTCAAAATAATTCGATTGCTGTACC 60
DB 354 GATAGTGTGTGTCGCCAAGGAAAATATATCCACCCCTCAAAATAATTCGATTGCTGTACC 413
QY 61 AAGTGGCAAGAGAACCTACTTCTACATGATGTCGAGCGCCGGGCGAGATACGGAC 120
DB 414 AAGTGGCAAGAGAACCTACTTCTACATGATGTCGAGCGCGCGGCGAGATACGGAC 473
QY 121 TGACGAGATCTTACACAGGCTTCTTTTCACCGCTTCAGAAACACCACTCAGACACTGCTC 180
DB 474 TGCACGAGATCTTACACAGGCTTCTTTTCACCGCTTCAGAAACACCACTCAGACACTGCTC 533
QY 181 AGCTGCTCCCAATGTGCAAAATCAAAATCAATGAGTCAAGTATCTTTCTTTCACAGCTGAC 240
DB 534 AGCTGCTCCCAATGTGCAAAATCAAAATCAATGAGTCAAGTATCTTTCTTTCACAGCTGAC 593
QY 241 CGAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 594 CGAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
QY 301 TTTCCAGTCTTTCAATTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 654 TTTCCAGTCTTTCAATTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
QY 361 AAAAGAAAGAGCTTGAATCTGATATGAGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 419
DB 714 AAAAGAAAGAGCTTGAATCTGATATGAGGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 773

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29	1	GAGGGTGTGTCCCAAGAAATATATACAGCCGCTCAATTAATGATTTGGTACG	60
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32		GGATGTTGTGTGTCCCAAGAAATATATACAGCCGCTCAATTAATGATTTGGTACG	
33	61	AGCGCGCAAAAGAAATGCTATTAACATATAGTATGCGCGCGCGCGCGATACGAC	120
34		AGCGCGCAAAAGAAATGCTATTAACATATAGTATGCGCGCGCGCGCGATACGAC	
35	121	TGCGCAAAAGAAATGCTATTAACATATAGTATGCGCGCGCGCGCGATACGAC	180
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 Best Local Similarity 99.2% Pred. No. 1.4e-130,  
 Matches 457; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

340 GATAGTGTGTGTCCTCCCAAGGAAAATATATATACACCTTCAAAAATAATTCGATTGCTTACC 399  
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 QY 121 TGAAGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGAG 180  
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 ACCESSION R1769006  
 VERSION R1769006  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 872)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
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 High quality sequence stop: 784.  
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 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
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 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dt  
 primed and directionally cloned (Ecopv site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Notes:  
 this is a NIH MGC Library."  
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 Best Local Similarity 97.3%; Pred. No. 1.7e 129;  
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 QY 121 TGAAGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGAGAGGAGTGTGAG 240  
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RESULT 15  
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 LOCUS AUI24446 NT2PM4 Homo sapiens cDNA clone NT2PM4860618 5', mRNA  
 REFERENCE AUI24446  
 ACCESSION AUI24446  
 VEPSTON AUI24446.1 GI:10949162  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 859)  
 Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, O.,  
 Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., and  
 Isogai, T.  
 HPI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,  
 Saito, K., Yamamoto, O., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki,  
 Y., Sugano, S., Isogai, T.)  
 Unpublished (2000)  
 Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yara, Fisarazu, Chiba 262 0412, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)

HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix Research Institute/ cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

## FEATURES

SOURCE

Location/Qualifiers

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 /note="Vector: pWE18SFU3, mRNA from uninduced NT2 neuronal precursor cells"

BASE COUNT 127 a 247 c 220 g 192 t 3 others

ORIGIN

## Query Match

30.54; Score 439; DB 9; Length 859;

Best Local Similarity 98.1%; Pred. No. 7,4e-129;

Matches 453; Conservative 0; Mismatches 8; Indels 1; Gaps 1,

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UY 61 AAGGCGTCAAAAGAAATCTTATATATCTGTGTGAGGCGGCGGCGGCGGCGGCGG 120
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UY 301 TCCAGTGTCCAAATGCGGAGTGGAGATGCGGAGTGGAGATGCGGAGTGGAGATGCG 360
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Search completed: January 6, 2003, 03:39:59  
 Job time : 2254 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: January 6, 2003, 03:45:53, Search time 33 seconds  
(without alignments)  
650.102 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 ISVLCQGYHPPQNNISHT CSNFFYSLETKLCPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	100.0	161	11	AAW27496 Native 30 kd TNF i
2	941	100.0	161	19	AAW59664 Human soluble tumo
3	941	100.0	161	19	AAW52267 Soluble tumour nec
4	941	100.0	161	20	AAW89233 Tumour necrosis in
5	941	100.0	161	22	AAW37676 Human 30 kDa TNF i
6	941	100.0	211	20	AAW89225 Tumour necrosis fa
7	941	100.0	280	22	AAW66976 Tnf1 protein in
8	941	100.0	309	16	AAW70108 TNF-R-G8PH fusion
9	941	100.0	311	20	AAW89229 Tumour necrosis fa
10	941	100.0	336	18	AAW33360 TBP(20-190)/hcg-be

11	941	100.0	366	20	AAW89228 Tumour necrosis fa
12	941	100.0	371	11	AAW07449 Tumour necrosis fa
13	941	100.0	377	20	AAW89227 Tumour necrosis fa
14	941	100.0	417	20	AAW89226 Tumour necrosis fa
15	941	100.0	420	16	AAW89224 Tumour necrosis fa
16	941	100.0	451	16	AAW70107 TNF R GRP 130 fusi
17	941	100.0	455	12	AAW10986 30kD TNF inhibitor
18	941	100.0	455	12	AAW11082 Human 30kD TNF kin
19	941	100.0	455	13	AAW20787 TNF alpha binding
20	941	100.0	455	13	AAW24090 TNF alpha ccd-1cc
21	941	100.0	455	14	AAW42059 Lambda derived TNF
22	941	100.0	455	16	AAW50844 p55 TNF R, Bm-1
23	941	100.0	455	20	AAW30934 Human tumour necro
24	941	100.0	455	21	AAW36266 Human tumour necro
25	941	100.0	455	21	AAW37800 Human tumour necro
26	941	100.0	455	21	AAW26084 Human TNFR 1, Bm
27	941	100.0	455	21	AAW23446 Human tumour necro
28	941	100.0	455	21	AAW01336 TNF R, death recep
29	941	100.0	455	22	AAW86817 Human TRFPP associ
30	941	100.0	455	22	AAW36697 Human tumour necro
31	941	100.0	455	22	AAW37677 Human 40 kDa TNF 1
32	941	100.0	455	23	AAW81649 Human tumour necro
33	941	100.0	455	23	AAW75064 Human tumour necro
34	941	100.0	547	16	AAW70104 TNF R GRP fusion
35	941	100.0	884	16	AAW70109 TNF R GRP 130 fusi
36	941	100.0	900	16	AAW70103 TNF R GRP 130 fusi
37	941	100.0	1245	16	AAW70106 TNF R p1, v1vax 1b
38	941	100.0	1604	16	AAW70105 TNF R ERA 176 fusi
39	938	99.7	455	11	AAW07451 Human Tumour Necro
40	932	99.0	433	14	AAW51032 Mutant p55 tumour
41	932	99.0	443	14	AAW51033 Mutant p55 tumour
42	932	99.0	455	14	AAW42197 p55 Tumour necrosi
43	932	99.0	455	14	AAW51034 Mutant p55 tumour
44	931	98.9	455	12	AAW12550 Type 1 TNF receptor
45	930.5	98.9	909	19	AAW64485 Human Fas protein

ALIGNMENTS

- RESULT 1  
AAW27496  
ID AAW27496 standard; protein; 161 AA.  
XX  
AC AAW27496;  
XX  
DT 09-MAR-1993 (first entry)  
XX  
DE Native 30 kd TNF inhibitor.  
XX  
KW Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
KW adult respiratory distress syndrome; rheumatoid arthritis;  
KW septic shock; pulmonary fibrosis; spacer.  
XX  
OS Homo sapiens  
XX  
PN W09216221-A.  
XX  
PD 01-OCT-1992.  
XX  
PF 13 MAR-1992; 92WO-US02122.  
XX  
PR 15-MAR-1991; 91US-0669462  
PR 17-JAN-1992; 92US-0822296.  
XX  
(SYND ) SYNERGEN INC.  
PI Armes LG, Brewer MT, Evans PJ, Kohno T, Thompson RC;  
XX  
WP1, 1992-348933/42.  
XX  
PT New ethylene glycolated polypeptide(s) with improved  
PT pharmacokinetic properties - for treating e.g. TNF and IL-1

mediated diseases, e.g. adult respiratory distress syndrome, rheumatoid arthritis, septic shock etc.

Claim 54; Fig 2; 100pp; English.

The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmacokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495.

Sequence 161 AA;

Query Match 100.0%; Score 941; DB 13; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWSENLFCQFNCSCLNGTVHLSQCE 120  
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1 KONTVCTCHAGFFLRENECVSCNCKKSLLECTKLCUPQIEN 161

#### RESULT 2

AAW59664 standard; Protein; 161 AA.

AAW59664;

28-SEP-1998 (first entry)

Human soluble tumour necrosis factor receptor type I.

Human; tumour necrosis factor; TNF; TNF receptor type I;

inflammatory disease; leukaemia; TNF binding protein;

anti-inflammatory drug; methotrexate.

Homo sapiens.

W09824463-A2.

11-JUN-1998.

08-DEC-1997; 97WO-US22733.

09-JUN-1997; 97US-0052023.

06-DEC-1996; 96US-0032587.

23-JAN-1997; 97US-0036355.

07-FEB-1997; 97US-0039315.

(AMGE-) AMGEN INC.

Bendele AM, Edwards CK, Sennello RM;

WP1; 1998-333039/29.

N-PSDB; AAW41548.

Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate

Disclosure; Fig 1; 104pp; English.

This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.

Sequence 161 AA;

Query Match 100.0%; Score 941; DB 19; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DSVCPGKGIHPQNNSTICTCKHKGTYLVNDGPGQDIDCEBESGFTASENHLRHCL 60  
1 DSVCPGKGIHPQNNSTICTCKHKGTYLVNDGPGQDIDCEBESGFTASENHLRHCL 60  
1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWSENLFCQFNCSCLNGTVHLSQCE 120  
1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWSENLFCQFNCSCLNGTVHLSQCE 120  
1 KONTVCTCHAGFFLRENECVSCNCKKSLLECTKLCUPQIEN 161  
1 KONTVCTCHAGFFLRENECVSCNCKKSLLECTKLCUPQIEN 161

#### RESULT 3

AAW52267 standard; Protein; 161 AA.

AAW52267;

29-JUN-1998 (first entry)

Soluble tumour necrosis factor receptor.

Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease;

tumour necrosis factor binding protein; autoimmune disease; arthritis;

adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;

chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.

Homo sapiens.

W09801555-A2.

15-JAN-1998.

09-JUL-1997; 97WO-US12244.

04-MAR-1997; 97US-0039792.

09-JUL-1996; 96US-0021443.

06-DEC-1996; 96US-0032534.

23-JAN-1997; 97US-0037737.

07-FEB-1997; 97US-0039314.

(AMGE-) AMGEN INC.

Edwards CK, Fisher EF, Kieft GL;

WP1; 1998-101052/09.

N-PSDB; AAV19801.

Truncated and soluble forms of tumour necrosis factor receptor -

useful for treating diseases involving factor, e.g. arthritis and

adult respiratory distress syndrome

Claim 1; Fig 1; 205pp; English.

This sequence is the human soluble tumour necrosis factor receptor (STNFR). The protein was used to make the truncated STNFR proteins of the invention. The truncated STNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant STNFR, which may also be used for measuring the amount of STNFR in samples and to raise antibodies against STNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The STNFR proteins are well suited to large scale production (since they lack the deamidation site in region III-136, so are more stable in vivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.

Query Match 100.0%; Score 941; DR 19; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSVCPQCKYHPPONNSICTGTHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60  
DB 1 DSVCPQCKYHPPONNSICTGTHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60  
QY 61 SCSKPFEMGQVEISSCTVDPRTVCGCPFNQVPHYWSNLEPQFNCLNGTVHLSQOE 120  
DB 61 SCSKPFEMGQVEISSCTVDPRTVCGCPFNQVPHYWSNLEPQFNCLNGTVHLSQOE 120  
QY 121 KQNTVCTCHAGFFIRFENFVCSNCFKSLCTYLCLDQIEN 161  
DB 121 KQNTVCTCHAGFFIRFENFVCSNCFKSLCTYLCLDQIEN 161

RESULT 4  
AAB37676  
ID AAB37676 standard; protein; 161 AA.  
XX AC AAB37676;  
XX DT 02-MAR-2001 (first entry)  
XX DE Human 30 kDa TNF inhibitor.  
XX KW Tumour necrosis factor receptor 1, TNFR-1; inhibitor; osteoprotegerin;  
XX KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
XX KW inflammation; apoptosis.  
XX OS Homo sapiens.  
XX PN W09849405.A1.  
XX PD 05-NOV-1998.  
XX PF 29-APR-1998; 98WO-0508631.  
XX PR 01-MAY-1997; 97US-0850188.  
XX PA (AMGE ) AMGEN INC.  
XX PI Boyle WT, Wooden S;  
XX XX WPI; 1999-014661/03.  
XX DR N-PSDB; AAV81732.  
XX XX New chimeric osteoprotegerin polypeptides - contain the  
XX PT osteoprotegerin dimerisation domain and a heterologous sequence,  
XX PT useful to treat TNF and TNFR-mediated disorders  
XX PS Disclosure; Fig 2; 92pp; English.  
XX XX The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents the TNF inhibitor 30 kDa protein.

XX Sequence 161 AA;  
Query Match 100.0%; Score 941; DR 20; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSVCPQCKYHPPONNSICTGTHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60  
DB 1 DSVCPQCKYHPPONNSICTGTHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60  
QY 61 SCSKPFEMGQVEISSCTVDPRTVCGCPFNQVPHYWSNLEPQFNCLNGTVHLSQOE 120  
DB 61 SCSKPFEMGQVEISSCTVDPRTVCGCPFNQVPHYWSNLEPQFNCLNGTVHLSQOE 120  
QY 121 KQNTVCTCHAGFFIRFENFVCSNCFKSLCTYLCLDQIEN 161  
DB 121 KQNTVCTCHAGFFIRFENFVCSNCFKSLCTYLCLDQIEN 161

RESULT 5  
AAB37676  
ID AAB37676 standard; protein; 161 AA.  
XX AC AAB37676;  
XX DT 02-MAR-2001 (first entry)  
XX DE Human 30 kDa TNF inhibitor.  
XX KW TNF inhibitor; antiinflammatory. Tumour Necrosis Factor; Interleukin;  
XX KW IL-1; inflammatory disease; degenerative disease; human.  
XX OS Homo sapiens.  
XX PN US6143866-A.  
XX PD 07-NOV-2000.  
XX PF 19-JAN-1995; 95US-0375242.  
XX PR 19-JUL-1990; 90US-0555274.  
XX PR 09-JUL-1993; 93US-0090366.  
XX PR 18-JUL-1989; 89US-0381080.  
XX PR 11-DEC-1989; 89US-0450329.  
XX PR 07-FER-1990; 90US-0479661.  
XX XX (AMGE-) AMGEN INC.  
XX XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC,  
XX XX Vanderslice RW, Vannice J, Kohno T;  
XX XX WPI; 2001-006443/01.  
XX XX N-PSDB; AAC83945.  
XX XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a  
XX PT non-native cysteine residue cross linked with polyethylene glycol,  
XX PT useful for treating inflammatory and degenerative diseases mediated by

PT TNF -  
 XX Claim 1: Fig 19; 82pp; English.  
 PS  
 CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors  
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The  
 CC novel TNF inhibitors of the present invention are useful as therapeutic  
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and  
 CC for treating inflammatory and degenerative diseases mediated by TNF. The  
 CC 30 kDa TNF inhibitor can inhibit TNF alpha  
 CC  
 XX  
 SQ Sequence 161 AA;  
 Query Match 100.0%; Score 941; DB 22; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 UY 1 DSVCPGKGYIHPNNNSICTCKHKGTYLYNDGPGQDDDCRCESGFTASENHLRHCL 60  
 DB 1 DSVCPGKGYIHPNNNSICTCKHKGTYLYNDGPGQDDDCRCESGFTASENHLRHCL 60  
 CY 61 SCSKCKKEMGQVEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 61 SCSKCKKEMGQVEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSQCE 120  
 CY 121 KQNTVCTCHAGFFLENECVSCNCKKSLCTKLCIPQIEN 161  
 DB 121 KQNTVCTCHAGFFLENECVSCNCKKSLCTKLCIPQIEN 161  
 RESULT 6  
 ID AAB89225  
 XX AAB89225 standard; Protein; 211 AA.  
 AC AAB89225;  
 DT 04-MAR-1999 (first entry)  
 XX  
 DE Tumour necrosis factor b2/osteoprotegerin construct TNFbp 4.0.  
 XX  
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN M09849305-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 29-APR-1998; 98WO-US06631.  
 XX  
 PR 01-MAY-1997; 9/US-0450194  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Wooden S;  
 XX WPI; 1999-034661/03.  
 DR WPI; 1999-034661/03.  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 PT  
 XX  
 XX Example 1; Fig 4; 92pp; English.  
 PS  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.  
 CC  
 XX  
 SQ Sequence 211 AA;  
 Query Match 100.0%; Score 941; DB 20; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DSVCPGKGYIHPNNNSICTCKHKGTYLYNDGPGQDDDCRCESGFTASENHLRHCL 60  
 DB 41 DSVCPGKGYIHPNNNSICTCKHKGTYLYNDGPGQDDDCRCESGFTASENHLRHCL 100  
 OY 61 SCSKCKKEMGQVEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 101 SCSKCKKEMGQVEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSQCE 160  
 OY 121 KQNTVCTCHAGFFLENECVSCNCKKSLCTKLCIPQIEN 161  
 DB 161 KQNTVCTCHAGFFLENECVSCNCKKSLCTKLCIPQIEN 201

RESULT 7  
 ID AAB66979  
 XX AAB66979 standard; Protein; 280 AA.  
 AC AAB66979;  
 DT 19-APR-2001 (first entry)  
 XX  
 DE Tnfr1 protein.  
 XX  
 KW Bone loss; osteoprotegerin, OPG, rheumatoid arthritis; hyperalgesia;  
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
 KW ischaemia; Parkinson's disease.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 PN W0200103719-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000WO-US18667.  
 XX  
 PR 09-JUL-1999; 99US-0350670.  
 XX  
 PR 09-DEC-1999; 99US-0457647.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Lacey DL, Calzone FU, Chang M, Senaldi G;  
 XX WPI; 2001-103031/11.  
 DR WPI; 2001-103031/11.  
 XX  
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
 PT multiple sclerosis and asthma, comprises administering an  
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of  
 PT interleukin and tumor necrosis factor alpha  
 XX  
 PS Disclosure; Fig 2; 316pp; English.  
 XX



The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAFS7836-AAFS7838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor- $\alpha$  (TNF- $\alpha$ ) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)-11 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock. The present sequence was used in a sequence homology comparison.

XX Sequence 280 AA;  
 Query Match 100.0%; Score 941; DB 22; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 4e-67;  
 Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISCTCTCHGTYLYNDQPGPGQDTCPCESGSFTASENHLPCL 60  
 DB 41 DSVCPQGYIHPQNNISCTCTCHGTYLYNDQPGPGQDTCPCESGSFTASENHLPCL 100  
 QY 61 SCSCPKPMQGVFISCTVDRTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSCOE 120  
 DB 101 SCSCPKPMQGVFISCTVDRTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSCOE 160  
 QY 121 KQNTVCTCHAGFFLPENECVSCNCKSLETCIKLCPQIEN 161  
 DB 161 KQNTVCTCHAGFFLPENECVSCNCKSLETCIKLCPQIEN 201

RESULT 8  
 AAR70108  
 ID AAR70108 standard; Protein; 309 AA  
 AC AAR70108;  
 DT 10 NOV 1995 (first entry)  
 DE TNF-R GRP fusion protein.  
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
 KW GRP 130; GRP; glycoprotein binding peptide homologue; glycoprotein A;  
 KW tumour necrosis factor receptor; TNF-R.  
 OS Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 FH Key Location/Qualifiers  
 FT Misc difference 230 269  
 FT /label= repeat\_region  
 FT /note= "can be repeated n times, where n is a real  
 number"

W09506737-A.  
 XX  
 XX 09 MAR 1995.  
 XX  
 XX 01 SEP 1994; 94WO-GB01900.  
 XX  
 XX 03 SEP 1994; 91GB-0018150  
 XX 23 AUG 1994; 94GB-0017021.  
 XX (PREN/) PRENDERCAST K F.  
 XX PA  
 XX Prondercast KF;

XX WPI; 1995-115452/15.  
 XX New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 FT a receptor peptide.  
 XX  
 PS Example A; Page 54-55; 93pp; English.  
 XX  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. AAR70108 25 are examples  
 CC of these hybrid peptides. AAR70108 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 461 469)  
 CC and glycoprotein binding protein (GPB) homologue (GRP). The  
 CC use of cytokine receptors not normally found on RBCs means that the  
 CC cytokine can bind harmlessly to the RBC without deleterious effect.  
 CC The RBC protects the hybrid peptides from excretion from the kidney, and  
 CC due to steric hindrance prevents the cytokines binding to a receptor in  
 CC another cell. GRP 130 or GRP are the pref. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
 CC PMWSA (pre major merozoite surface antigen) and the puffy binding  
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
 CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on the  
 CC surface of RBCs. The hybrid peptides are thus used to lower the levels of  
 CC free cytokines in the circulation to reduce pathological damage.

SQ Sequence 309 AA;

Query Match 100.0%; Score 941; DB 16; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-67;  
 Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISCTCTCHGTYLYNDQPGPGQDTCPCESGSFTASENHLPCL 60  
 DB 20 DSVCPQGYIHPQNNISCTCTCHGTYLYNDQPGPGQDTCPCESGSFTASENHLPCL 79  
 QY 61 SCSCPKPMQGVFISCTVDRTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSCOE 120  
 DB 80 SCSCPKPMQGVFISCTVDRTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSCOE 139  
 QY 121 KQNTVCTCHAGFFLPENECVSCNCKSLETCIKLCPQIEN 161  
 DB 140 KQNTVCTCHAGFFLPENECVSCNCKSLETCIKLCPQIEN 180

RESULT 9  
 AAR89229  
 ID AAR89229 standard; Protein; 311 AA.  
 XX  
 AC AAR89229;  
 XX  
 DT 04-MAR-1999 (first entry)  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.  
 XX  
 KW Tumour necrosis factor receptor 1, TNF- $\alpha$  1, inhibitory; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX W09849305-A1.  
 XX  
 XX 05-NOV-1998.  
 XX  
 XX 29-APR-1998; 98WO-US08631.  
 XX  
 XX 01-MAY-1997; 97US-0850188.  
 XX  
 XX PA  
 XX (AMGE-) AMGEN INC.

PI Boyle WJ, Wooden S;  
 XX  
 DR WPI, 1999 034661/03.  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Example 1, Fig 4, 30pp; English.  
 XX  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFR/OPG construct from  
 CC the cDNA of the present invention for creating TNFR/OPG fusion  
 CC proteins.  
 XX  
 SQ Sequence 311 AA;  
 Query Match 100.0%; Score 941; DB 29; Length 311;  
 Best Local Similarity 100.0%, Freq. No. 4, 4e-67,  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVFPGGKVIHPQNNISICTCKKQTYLVNMGPGPQDTDCRECEGSPFASENHLRCL 60  
 DB 23 DSVCFQGGYTHFGNNSICTCKKQKTYLVNDCGPGDDIDCEGSGFASENHLRCL 62  
 QY 61 SCSCGRKEMGVLEISCTVDRTVCCGRKNQYHWSNLPQCFNCSLCLNTVHLSCE 120  
 DB 83 SSSRFEMGVLEISCTVDRTVCCGRKNQYHWSNLPQCFNCSLCLNTVHLSCE 142  
 QY 11 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 161  
 DB 11 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 183  
 QY 101 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 161  
 DB 101 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 201  
 DE 19 MAR-1998 (first entry)  
 QY TRP120-180/hcg-beta fusion protein  
 DE TRP120-180/hcg-beta fusion protein  
 XX Fused protein, hcg-beta-fusion; TPO, human chorionic gonadotropin;  
 KM beta subunit; hcg-beta.  
 XX Homo sapiens  
 XX MO9730161-A1.  
 XX 21-AUG-1997.  
 PD 20-FEB-1997; 97WO-US02315.  
 XX 20-FEB-1997; 96US-0011936.  
 XX 20-FEB-1996; 96US-0011936.  
 EA (VICT) AIDS AFFLIED FFS SYSTEMS HOLDING INC  
 XX Campbell PK, Chapel SQ, Jamison BA,  
 PI

XX WPI, 1997-425036/39.  
 DR N PSDB; AAT94022.  
 XX  
 PT Hybrid dimeric protein comprising two co-expressed units - each  
 PT based on receptor or ligand and a subunit of a heterodimeric  
 PT hormone, especially FSH, for inducing follicular maturation  
 XX  
 PS Example; Pages 39-40; 60pp; English.  
 XX  
 CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
 CC acid sequences, each consisting of a homodimeric or heterodimeric  
 CC receptor chain or ligand, with ligand-receptor binding activity,  
 CC bound directly or via a peptide linker to a subunit of a  
 CC heterodimeric protein hormone capable of forming a heterodimer with  
 CC the hormone's other subunits. The fusion protein, e.g. the  
 CC thymopoietin (TPO)/human chorionic gonadotropin-beta subunit  
 CC (hcg-beta) fusion protein denoted by the present sequence,  
 CC significantly increases the biological activity of the hormone  
 CC component, reducing the requirement for hormone itself and the  
 CC number of injections needed.  
 XX  
 SQ Sequence 336 AA;  
 Query Match 100.0%; Score 941; DB 18; Length 336;  
 Best Local Similarity 100.0%, Freq. No. 4, 7e-67,  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVFPGGKVIHPQNNISICTCKKQTYLVNMGPGPQDTDCRECEGSPFASENHLRCL 60  
 DB 23 DSVCFQGGYTHFGNNSICTCKKQKTYLVNDCGPGDDIDCEGSGFASENHLRCL 62  
 QY 61 SCSCGRKEMGVLEISCTVDRTVCCGRKNQYHWSNLPQCFNCSLCLNTVHLSCE 120  
 DB 83 SSSRFEMGVLEISCTVDRTVCCGRKNQYHWSNLPQCFNCSLCLNTVHLSCE 142  
 QY 11 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 161  
 DB 11 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 183  
 QY 101 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 161  
 DB 101 KNTVCTGHAQFLRENECVSGNCRKSLCTKLPQLEN 201  
 DE 04-MAR-1999 (first entry)  
 QY Tumour necrosis factor bp/osteoprotegerin construct TNFR/248.  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFR/248.  
 XX Tumour necrosis factor receptor 1, TNFR-1; inhibitor, osteoprotegerin,  
 KM OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KM inflammation; apoptosis.  
 XX Homo sapiens.  
 XX Synthetic.  
 XX MO9849305-A1.  
 XX 05-NOV-1998.  
 XX 29-APR-1998; 98WO-US08631.  
 XX 01-MAY-1997; 97US-0850188.  
 XX (AMGE-) AMGEN INC.  
 XX Boyle WJ, Wooden S;  
 XX WPI, 1999 034661/03.  
 PT New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.

XX Sequence 366 AA;

Query Match 100.0%; Score 941; DB 20; Length 366;  
Best Local Similarity 100.0%; Pred. No. 5, 1e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 60  
DB 41 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 100  
QY 61 SCSCPFPMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNGLCLNGTIVHLSCQE 120  
DB 101 SCSCPFPMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNGLCLNGTIVHLSCQE 160  
QY 121 KONTVCTCHAGFFPERFVSCNCFKYSLEPTCLCLPQIEN 161  
DB 161 KONTVCTCHAGFFPERFVSCNCFKYSLEPTCLCLPQIEN 201

RESULT 12

AAR07449  
ID AAR07449 standard; protein; 371 AA.

XX AAR07449;

XX 29 JAN-1991 (first entry)

DE Tumour Necrosis Factor Binding Protein from pTNF-BP15 cDNA.

XX Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KW pTNF BP15; infectious disease; parasitic disease; cachexia;  
KW autoimmune disease; shock.

XX Homo sapiens.

XX EP393438 A.

XX 24 OCT 1990.

XX 06-APR 1990; 90EP-0106624.

XX 21 JUN-1989; 89DE 3920282.

XX 21 APR 1989; 89DE-3913101.

XX (BOEH ) ROEHRINGER INGELHEIMINT.

XX Hauptmann R, Himmler A, Maurer-Fogy I, Stratawa C;

XX WPI; 1990-321987/43.

XX N-PSNR; AAQ06282.

XX DNA encoding TNF binding protein and TNF receptor used in  
PT tumour treatment and to understand mechanism to TNF action

XX Disclosure; Fig 1(1-3); 51pp; German.

XX Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of  
CC e.g. COS7 cells. The expressed proteins are useful  
CC prophylactically and therapeutically to control disorders which  
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
CC respiratory distress syndrome etc.), or side effects of treatment with  
CC TNF-alpha). They can also be used as diagnostic reagents for  
CC assaying TNF and in study of TNF-receptor interactions.  
XX See also AAQ06282-Q06285.

XX Sequence 371 AA;

Query Match 100.0%; Score 941; DB 11; Length 371;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 60  
DB 41 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 100  
QY 61 SCSCPFPMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNGLCLNGTIVHLSCQE 120  
DB 101 SCSCPFPMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNGLCLNGTIVHLSCQE 160  
QY 121 KONTVCTCHAGFFPERFVSCNCFKYSLEPTCLCLPQIEN 161  
DB 161 KONTVCTCHAGFFPERFVSCNCFKYSLEPTCLCLPQIEN 201

RESULT 13

AAW89227

ID AAW89227 standard; Protein, 297 AA.

XX AAW89227;

XX 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin  
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
KW inflammation; apoptosis.

XX Homo sapiens.

XX Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,

PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFp/OPG construct from the example of the present invention for creating TNFp/OPG fusion proteins.

Sequence 397 AA;

Query Match 100.0%, Score 341, DB 20, Length 397;  
Best Local Similarity 100.0%, Pred. No. 5, 8e-67,  
Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

1 DSVCPQKRYIHPONNSTICTCKRKGYLYNDGPGQDDDCRECSGFTASENHRLCL 60  
41 DSVCPQKRYIHPONNSTICTCKRKGYLYNDGPGQDDDCRECSGFTASENHRLCL 100  
61 SCSCRKEMQVEISSCTVDRDVQSGPKQVPHWSENLFCQFNLSLCLNTVHLSQCE 120  
101 SCSCRKEMQVEISSCTVDRDVQSGPKQVPHWSENLFCQFNLSLCLNTVHLSQCE 160  
121 KQNTVCTCHAGFFLRNECVSCSNCKKSLBCTKLCLEPQLEN 161  
161 KQNTVCTCHAGFFLRNECVSCSNCKKSLBCTKLCLEPQLEN 201

RESULT 14

AAW89226  
ID AAW89226 standard; Protein: 417 AA.

AC AAW89226;  
DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor lg/osteoprotegerin construct TNFp/196.

FM Tumour necrosis factor receptor 1, TNFR 1, inhibitor, osteoprotegerin;  
OR OPG, chimeric, fusion, dimerisation domain, autoimmune disease;  
KW inflammation; apoptosis.

CS Homo sapiens.  
CS Synthetic.

PN WO9849305-A1.

PD 05-NOV-1998.

PF 29-APR-1998; 98WO-US08631.

PR 01-MAY-1997; 97US-0850188.

PA (AMGE-) AMGEN INC.

PI Boyle WJ, Wooden S;

WI; 1999-034661/03.

New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

Example 1; Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFp/OPG construct from the example of the present invention for creating TNFp/OPG fusion proteins.

Sequence 417 AA;

Query Match 100.0%, Score 341; DB 20, Length 417;  
Best Local Similarity 100.0%, Pred. No. 5, 8e-67,  
Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

1 DSVCPQKRYIHPONNSTICTCKRKGYLYNDGPGQDDDCRECSGFTASENHRLCL 60  
41 DSVCPQKRYIHPONNSTICTCKRKGYLYNDGPGQDDDCRECSGFTASENHRLCL 100  
61 SCSCRKEMQVEISSCTVDRDVQSGPKQVPHWSENLFCQFNLSLCLNTVHLSQCE 120  
101 SCSCRKEMQVEISSCTVDRDVQSGPKQVPHWSENLFCQFNLSLCLNTVHLSQCE 160  
121 KQNTVCTCHAGFFLRNECVSCSNCKKSLBCTKLCLEPQLEN 161  
161 KQNTVCTCHAGFFLRNECVSCSNCKKSLBCTKLCLEPQLEN 201

RESULT 15

AAW89224  
ID AAW89224 standard; Protein: 420 AA.

AC AAW89224;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFp/OPG.

FM Tumour necrosis factor receptor 1, TNFR 1, inhibitor, osteoprotegerin;  
OR OPG, chimeric, fusion, dimerisation domain, autoimmune disease;  
KW inflammation; apoptosis.

CS Homo sapiens.  
CS Synthetic.

PN WO9849305-A1.

PD 05-NOV-1998.

PF 29-APR-1998; 98WO-US08631.

PR 01-MAY-1997; 97US-0850188.

PA (AMGE-) AMGEN INC.

PI Boyle WJ, Wooden S;

WI; 1999-034661/03.

New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.  
XX SQ Sequence 420 AA;  
Query Match 100.0%; Score 941; DB 20; Length 420;  
Rest Local Similarity 100.0%; Pred. No 5.8e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSVCTQGRVYHPQNNISICTKHKTLYLNDPCPGQDTDCPECSGFTASENHLPHCL 60  
DB 41 DSVCTQGRVYHPQNNISICTKHKTLYLNDPCPGQDTDCPECSGFTASENHLPHCL 100  
QY 61 SCSEKPKEMQGVFISSTVDGNTVCGEPKQYPHYWSENLPQCNCSLCLNGTVHLSQCE 120  
DB 101 SCSEKPKEMQGVFISSTVDGNTVCGEPKQYPHYWSENLPQCNCSLCLNGTVHLSQCE 160  
QY 121 KONTVCTCHAGPFLRENECVSCNCKSLECTKLCLPOIEN 161  
DB 161 KONTVCTCHAGPFLRENECVSCNCKSLECTKLCLPOIEN 201

Search completed: January 6, 2003, 03:57:45  
Job time : 41 secs



GenCore version 5.1.3  
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OM protein protein search, using sw model

Run on: January 6, 2003, 03:57:07 / Search time 17 Seconds  
(without alignments)  
278.652 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQGYIHQNNISICT . . . CSNCKYSUECTLCLEQIEN 161

Scoring table: BLOSUM62

Gapop 10 0 . Gapext 0 5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cqn2\_6/prodata/1/iaa/5A.COMB.pep.\*  
2: /cqn2\_6/prodata/1/iaa/5R.COMB.pep.\*  
3: /cqn2\_6/prodata/1/iaa/6A.COMB.pep.\*  
4: /cqn2\_6/prodata/1/iaa/6R.COMB.pep.\*  
5: /cqn2\_6/prodata/1/iaa/pCTUS.COMB.pep.\*  
6: /cqn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	161	US 09 326-394.2	Sequence 2, Appl
2	941	100.0	280	US-08-974-022-46	Sequence 46, Appl
3	941	100.0	280	US-08-795-445A-46	Sequence 46, Appl
4	941	100.0	280	US-08-795-447A-46	Sequence 46, Appl
5	941	100.0	280	US-08-974-186-46	Sequence 46, Appl
6	941	100.0	280	US-08-795-446B-46	Sequence 46, Appl
7	941	100.0	280	US-08-706-945D-132	Sequence 132, App
8	941	100.0	336	US-08-804-166-8	Sequence 8, Appl
9	941	100.0	336	US-08-910-991-8	Sequence 8, Appl
10	941	100.0	455	US-08-050-319B-25	Sequence 25, Appl
11	941	100.0	455	US-08-321-668-2	Sequence 2, Appl
12	941	100.0	455	US-08-837-941-2	Sequence 2, Appl
13	941	100.0	455	US-08-126-016-2	Sequence 2, Appl
14	941	100.0	455	US-08-465-982-25	Sequence 25, Appl
15	941	100.0	455	US-08-815-469-5	Sequence 5, Appl
16	941	100.0	455	US-09-006-353A-3	Sequence 3, Appl
17	941	100.0	455	US-09-527-236A-5	Sequence 5, Appl
18	941	100.0	455	US-08-054-970-2	Sequence 2, Appl
19	941	100.0	455	US-08-565-918-4	Sequence 4, Appl
20	941	100.0	455	US-09-573-986-3	Sequence 3, Appl
21	930.5	98.9	909	US-09-013-895A-4	Sequence 4, Appl
22	930.5	98.9	909	US-09-448-868-4	Sequence 4, Appl
23	928	98.6	285	US-08-804-166-6	Sequence 6, Appl
24	928	98.6	285	US-08-910-991-6	Sequence 6, Appl
25	925.5	98.4	453	US-09-086-483A-5	Sequence 5, Appl
26	924	98.2	199	US-08-050-319B-48	Sequence 48, Appl
27	924	98.2	199	US-08-465-982-48	Sequence 48, Appl

28	921	97.9	197	4	US-08-828-683A-21	Sequence 21, Appl
29	904	96.1	154	4	US-08-828-683A-12	Sequence 12, Appl
30	900	95.6	153	2	US-08-219-237B-4	Sequence 4, Appl
31	900	95.6	153	4	US-08-477-347-12	Sequence 12, Appl
32	900	95.6	153	4	US-08-476-862-3	Sequence 4, Appl
33	900	95.6	153	4	US-08-468-560C-4	Sequence 4, Appl
34	873	92.8	154	2	US-08-232-087A-10	Sequence 10, Appl
35	842.5	89.5	256	4	US-08-804-166-2	Sequence 2, Appl
36	842.5	89.5	256	4	US-08-910-991-2	Sequence 2, Appl
37	837	88.9	307	4	US-08-804-166-4	Sequence 4, Appl
38	837	88.9	307	4	US-08-910-991-4	Sequence 4, Appl
39	822	87.4	139	4	US-08-706-945D-129	Sequence 129, App
40	746	79.3	167	1	US-08-050-319B-2	Sequence 2, Appl
41	746	79.3	167	1	US-08-050-319B-57	Sequence 57, Appl
42	746	79.3	167	2	US-08-465-982-2	Sequence 2, Appl
43	746	79.3	167	2	US-08-465-982-57	Sequence 57, Appl
44	731	77.7	124	1	US-08-050-319B-4	Sequence 4, Appl
45	731	77.7	124	2	US-08-465-982-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-326-394-2  
; Sequence 2, Application US/09326394  
; Patent No. 6306820  
; GENERAL INFORMATION:  
; APPLICANT: Bendelle, Alison M.  
; APPLICANT: Sennello, Regina M.  
; APPLICANT: Edwards, Carl K.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TGF BINDING  
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,587  
; FILING DATE: 06 DEC 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,355  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07 FEB 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/052,023  
; FILING DATE: 09-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zindrick, Thomas K.  
; REGISTRATION NUMBER: 32,185  
; REFERENCE/DOCKET NUMBER: A-430D  
; INFORMATION FOR SEQ ID NO. 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-326-394-2

Query Match 100.0%, Score 941, DB 4, Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 DSVCPQCKYIHPQNNISICTKCHKGYLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
DB 1 DSVCPQCKYIHPQNNISICTKCHKGYLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
UY 61 SCSKCKEMGQVEISSCTVDRDVTGCGCKKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
DB 61 SCSKCKEMGQVEISSCTVDRDVTGCGCKKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
UY 121 KONTVCTCHAGFFLENECVSCNCKKSLECTKLCIPIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKKSLECTKLCIPIEN 161

## RESULT 2

US-08-974-022-46  
Sequence 46, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Denavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wintner, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022 46

Query Match 100.0%; Score 941; DB 3; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 DSVCPQCKYIHPQNNISICTKCHKGYLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
DB 41 DSVCPQCKYIHPQNNISICTKCHKGYLYNDGPGQDDDCRECEGSGFTASENHLRHCL 100  
UY 61 SCSKCKEMGQVEISSCTVDRDVTGCGCKKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
DB 101 SCSKCKEMGQVEISSCTVDRDVTGCGCKKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 160  
UY 121 KONTVCTCHAGFFLENECVSCNCKKSLECTKLCIPIEN 161

DB 161 KONTVCTCHAGFFLENECVSCNCKKSLECTKLCIPIEN 201

## RESULT 3

US-08-795-445A-46  
Sequence 46, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Denavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wintner, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-445A-46

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 DSVCPQCKYIHPQNNISICTKCHKGYLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
DB 41 DSVCPQCKYIHPQNNISICTKCHKGYLYNDGPGQDDDCRECEGSGFTASENHLRHCL 100  
UY 61 SCSKCKEMGQVEISSCTVDRDVTGCGCKKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
DB 101 SCSKCKEMGQVEISSCTVDRDVTGCGCKKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 160  
UY 121 KONTVCTCHAGFFLENECVSCNCKKSLECTKLCIPIEN 161  
DB 161 KONTVCTCHAGFFLENECVSCNCKKSLECTKLCIPIEN 201

## RESULT 4

US-08-795-447A-46  
Sequence 46, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin



```

; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-37402
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A 46
;
; Query Match 100.0%; Score 941; DB 4; Length 280;
; Best Local Similarity 100.0%; Pred. No. 2.7e-76;
; Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DSVCPQGGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 60
; DB 41 DSVCPQGGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 100
;
; QY 61 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 120
; DB 101 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 160
;
; QY 121 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 161
; DB 161 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 201
;
; RESULT 5
; US 08 974 186-46
; Sequence 46, Application US/08974186
; Patent No. 6,284,740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTROPPOTEGEPIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-46
;
; Query Match 100.0%; Score 941; DB 4; Length 280;
; Best Local Similarity 100.0%; Pred. No. 2.7e-76;
; Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DSVCPQGGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 60
; DB 41 DSVCPQGGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 100
;
; QY 61 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 120
; DB 101 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 160
;
; QY 121 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 161
; DB 161 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 201
;
; RESULT 6
; US-08-795-446B-46
; Sequence 46, Application US/08795446B
; Patent No. 628032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTROPPOTEGEPIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-446B-46

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Query Match 100.0%, Score 941, DB 4, Length 280;  
 Best Local Similarity 100.0%, Pred No. 2 7e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DSVCPQGXIHPONNISICTKCHKGTLYNDPCPGQDTCRCESGSPFASENHLRHCL 60  
 DB 41 DSVCPQGXIHPONNISICTKCHKGTLYNDPCPGQDTCRCESGSPFASENHLRHCL 100  
 CY 61 SCSKCRKMGQVEISSCTVDRDVTVCGRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 101 SCSKCRKMGQVEISSCTVDRDVTVCGRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 160  
 CY 121 KONTVCTCHAGFLFLENBECVSCSNCKKSECTYLCIPQIEN 161  
 DB 161 KONTVCTCHAGFLFLENBECVSCSNCKKSECTYLCIPQIEN 201

RESULT 7  
 US-08-706-945D-132  
 Sequence 132, Application US/970645D  
 Patent No. 6369027  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William  
 APPLICANT: Lacey, David  
 APPLICANT: Calzone, Frank  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: Osteoprotegerin  
 FILE REFERENCE: A-378CIP  
 CURRENT APPLICATION NUMBER: US/08/706,945D  
 CURRENT FILING DATE: 1996-09-03  
 PRIOR APPLICATION NUMBER: 08/577,788  
 PRIOR FILING DATE: 1995-12-22  
 NUMBER OF SEQ ID NOS: 145  
 SOFTWARE: Patent in version 3.1  
 SEQ ID NO 132  
 LENGTH: 280  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-706-945D-132

Query Match 100.0%, Score 941, DB 4, Length 280;  
 Best Local Similarity 100.0%, Pred No. 2 7e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DSVCPQGXIHPONNISICTKCHKGTLYNDPCPGQDTCRCESGSPFASENHLRHCL 60  
 DB 41 DSVCPQGXIHPONNISICTKCHKGTLYNDPCPGQDTCRCESGSPFASENHLRHCL 100  
 CY 61 SCSKCRKMGQVEISSCTVDRDVTVCGRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 101 SCSKCRKMGQVEISSCTVDRDVTVCGRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 160  
 CY 121 KONTVCTCHAGFLFLENBECVSCSNCKKSECTYLCIPQIEN 161  
 DB 161 KONTVCTCHAGFLFLENBECVSCSNCKKSECTYLCIPQIEN 201

RESULT 8  
 US-08-804-166-8  
 Sequence 8, Application US/08804166.  
 Patent No. 6193972  
 GENERAL INFORMATION:  
 APPLICANT: Campbell, Robert K.  
 APPLICANT: Jameson, Bradford A.  
 APPLICANT: Chapel, Scott C.  
 TITLE OF INVENTION: HYBRID PROTEINS  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: HOWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.

COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/804,166  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/011,936  
 FILING DATE: 20 February 1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Browdy, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: CAMPBELL=2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 336 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-804-166-8

Query Match 100.0%, Score 941, DB 4, Length 336;  
 Best Local Similarity 100.0%, Pred No. 3 2e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DSVCPQGXIHPONNISICTKCHKGTLYNDPCPGQDTCRCESGSPFASENHLRHCL 60  
 DB 23 DSVCPQGXIHPONNISICTKCHKGTLYNDPCPGQDTCRCESGSPFASENHLRHCL 82  
 CY 61 SCSKCRKMGQVEISSCTVDRDVTVCGRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 83 SCSKCRKMGQVEISSCTVDRDVTVCGRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 142  
 CY 121 KONTVCTCHAGFLFLENBECVSCSNCKKSECTYLCIPQIEN 161  
 DB 143 KONTVCTCHAGFLFLENBECVSCSNCKKSECTYLCIPQIEN 183

RESULT 9  
 US-08-910-991-8  
 Sequence 8, Application US/08910991  
 Patent No. 6194177  
 GENERAL INFORMATION:  
 APPLICANT: Campbell, Robert K.  
 APPLICANT: Jameson, Bradford A.  
 APPLICANT: Chapel, Scott C.  
 TITLE OF INVENTION: HYBRID PROTEINS  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,991  
 FILING DATE:  
 CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 747-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US 08 910-991-8

Query Match 100.0%; Score 941; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.2e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCTQCKYIHPQNNISCTCTCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 60
DB 23 DAVCTQCKYIHPQNNISCTCTCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 62
QY 61 SCSKPKFMQGVFISSTVDRTVCGPKNQYHYWSENLFQCFNCSLCLNGTVHLSQCE 120
DB 83 SCSKPKFMQGVFISSTVDRTVCGPKNQYHYWSENLFQCFNCSLCLNGTVHLSQCE 142
QY 121 KNTVCTCHAGFFLRENECVSCNCKESLCTKLCPLQIEN 161
DB 143 KNTVCTCHAGFFLRENECVSCNCKESLCTKLCPLQIEN 193

RESULT 10
US 08-050-3198-25
; Sequence 25, Application US/080503198
; Patent No. 5613145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P. W. Gray.
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Robert A L
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-321-668-2

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; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-050-3198-25

Query Match 100.0%; Score 941; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCTQCKYIHPQNNISCTCTCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 60
DB 41 DSVCTQCKYIHPQNNISCTCTCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 100
QY 61 SCSKPKFMQGVFISSTVDRTVCGPKNQYHYWSENLFQCFNCSLCLNGTVHLSQCE 120
DB 101 SCSKPKFMQGVFISSTVDRTVCGPKNQYHYWSENLFQCFNCSLCLNGTVHLSQCE 160
QY 121 KNTVCTCHAGFFLRENECVSCNCKESLCTKLCPLQIEN 161
DB 161 KNTVCTCHAGFFLRENECVSCNCKESLCTKLCPLQIEN 201

RESULT 11
US-08-321-668-2
; Sequence 2, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAEBUSCH, Cord
; APPLICANT: VARFLOMBEV, Eugene
; APPLICANT: BATYIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEEDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. No. 4.3e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 DSVFPGKVIHPNNSTICTKCKATVLYNDGPGQATDUCRECESSFTASENHLPHCL 60  
DB 41 DSVFPGKVIHPNNSTICTKCKATVLYNDGPGQATDUCRECESSFTASENHLPHCL 100  
CY 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 120  
DB 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 160  
CY 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 161  
DB 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 201  
RESULT 12  
US-08-837-941-2  
Sequence 2, Application US/08837941  
Patent No. 5766917  
GENERAL INFORMATION  
APPLICANT: WALLACH, David  
APPLICANT: EPPENBERG, Carl  
APPLICANT: VAPOLMEYEV, Eugene  
APPLICANT: BARKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TGF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENT ADDRESS  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/MS-WINDOWS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,941  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,668  
FILING DATE: 12 OCT-1994  
APPLICATION NUMBER: 11,107,068  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-941-2

Query Match 100.0%; Score 941; DB 1; Length 455;  
Best local Similarity 100.0%; Pred. 4.3e 76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DSVFPGKVIHPNNSTICTKCKATVLYNDGPGQATDUCRECESSFTASENHLPHCL 60  
DB 41 DSVFPGKVIHPNNSTICTKCKATVLYNDGPGQATDUCRECESSFTASENHLPHCL 100  
CY 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 120  
DB 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 160

DB 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 160  
CY 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 161  
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 201

RESULT 13  
US-08-126-016-2  
Sequence 2, Application US/08126016  
Patent No. 5811261  
GENERAL INFORMATION:  
APPLICANT: WALLACH, DAVID  
APPLICANT: NOHAR, YARON  
APPLICANT: KEMPER, OLIVER  
APPLICANT: ENGELMANN, HARTMUT  
APPLICANT: BRAKEBUSCH, CORD  
APPLICANT: ADERKA, DAN  
TITLE OF INVENTION: EXPRESSION OF THE PEROMYELITIS TUMOR  
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TFP-I)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,016  
FILING DATE: 24-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/625668  
FILING DATE: 13-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, ROGER L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-126-016-2

Query Match 100.0%; Score 941; DB 2; Length 455;  
Best local Similarity 100.0%; Pred. 4.3e 76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DSVFPGKVIHPNNSTICTKCKATVLYNDGPGQATDUCRECESSFTASENHLPHCL 60  
DB 41 DSVFPGKVIHPNNSTICTKCKATVLYNDGPGQATDUCRECESSFTASENHLPHCL 100  
DB 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 120  
CY 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 160  
DB 101 SCSPKPEPMQVEISSCTVDPDTVGGPRQYRWYSENLFQCFNCSCLNGTVHLSQCE 161  
CY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 161  
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIEN 201

RESULT 14  
US 08 465-982-25  
Sequence 25, Application US/08465982  
Patent No. 5863786  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 615 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,982  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319  
FILING DATE: 10-May-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Robert L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US 08 465-982-25  
Query Match 100.0%; Score 941; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKCHKTYLYNDGPGQDTPCEGSGSFTASENHLPHCL 60  
DB 41 DSVCPQGYIHPQNNISICTKCHKTYLYNDGPGQDTPCEGSGSFTASENHLPHCL 100  
QY 61 SCSKCPKEMGQVEISSCTVDFRTVCGCPFNQYHYWSENLFQCFNCSCLNGTIVHLSQCE 120  
DB 101 SCSKCPKEMGQVEISSCTVDFRTVCGCPFNQYHYWSENLFQCFNCSCLNGTIVHLSQCE 160  
QY 121 KONTVCTCHAGFFLEPENEVCSSNCKYSLETKLCPLQIEN 161  
DB 161 KONTVCTCHAGFFLEPENEVCSSNCKYSLETKLCPLQIEN 201

RESULT 15  
US 08 815-469-5  
Sequence 5, Application US/08815469  
Patent No. 6153402  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ni, Jian  
APPLICANT: Dixit, Vishva  
APPLICANT: Gentz, Reiner L.  
APPLICANT: Dillon, Patrick J.  
TITLE OF INVENTION: Death Domain Containing Receptors  
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,469  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 6153402 Yet Assigned  
FILING DATE: 06-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,711  
FILING DATE: 17-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,285  
FILING DATE: 12-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KPM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-815-469-5

Query Match 100.0%; Score 941; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKCHKTYLYNDGPGQDTPCEGSGSFTASENHLPHCL 60  
DB 41 DSVCPQGYIHPQNNISICTKCHKTYLYNDGPGQDTPCEGSGSFTASENHLPHCL 100  
QY 61 SCSKCPKEMGQVEISSCTVDFRTVCGCPFNQYHYWSENLFQCFNCSCLNGTIVHLSQCE 120  
DB 101 SCSKCPKEMGQVEISSCTVDFRTVCGCPFNQYHYWSENLFQCFNCSCLNGTIVHLSQCE 160  
QY 121 KONTVCTCHAGFFLEPENEVCSSNCKYSLETKLCPLQIEN 161  
DB 161 KONTVCTCHAGFFLEPENEVCSSNCKYSLETKLCPLQIEN 201

Search completed: January 6, 2003, 04:00:13  
Job time : 27 secs





DB 61 SCSSKREMGQVEIISCTVDRDVTGCGKKNQRYHWSENLFQCFNCSLCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
RESULT 2  
US-09-899-429A-4  
Sequence 4, Application US/09899429A  
Patent No. US2002016918A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98,385-J  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 06/477,639  
PRIOR FILING DATE: 1985-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-429A-4  
Query Match 100.0%; Score 941; DB 9; Length 161;  
Best Local Similarity 100.0%; Pred No. 2 8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
DB 61 SCSSKREMGQVEIISCTVDRDVTGCGKKNQRYHWSENLFQCFNCSLCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
RESULT 3  
US-09-792-356-4  
Sequence 4, Application US/09792356  
Patent No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98,385-G  
CURRENT APPLICATION NUMBER: US/09/792,356  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 08/477,639

DB 61 SCSSKREMGQVEIISCTVDRDVTGCGKKNQRYHWSENLFQCFNCSLCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
RESULT 4  
US-09-899-422-4  
Sequence 4, Application US/09899422  
Patent No. US20020090676A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98,385-H  
CURRENT APPLICATION NUMBER: US/09/899,422  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-422-4  
Query Match 100.0%; Score 941; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred No. 2 8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
DB 61 SCSSKREMGQVEIISCTVDRDVTGCGKKNQRYHWSENLFQCFNCSLCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRSLECTCTLCPLQIEN 161  
RESULT 5  
US-09-792-356-4  
Sequence 4, Application US/09792356  
Patent No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98,385-G  
CURRENT APPLICATION NUMBER: US/09/792,356  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 08/477,639



QY 61 SCSCPKFEMQVEISSCTVDRDTGCGKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
Db 61 SCSCPKFEMQVEISSCTVDRDTGCGKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 121 KQNTVCTCHAGFFLEPNECVSNCNFKKSECTKLCLOPIEN 161  
Db 121 KQNTVCTCHAGFFLEPNECVSNCNFKKSECTKLCLOPIEN 161

RESULT 5  
US-09 907-263-2  
Sequence 2, Application US/0907263  
Patent No. US20020119924A1  
GENERAL INFORMATION:  
APPLICANT: Bendele, Alison M.  
Sennello, Regina M.  
Edwards, Carl K.  
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
PROTEIN FOR TREATING TNF-MEDIATED DISEASES

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: US  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/907,263  
FILING DATE: 17-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/326,394  
FILING DATE: 1999-06-04  
APPLICATION NUMBER: US 60/036,355  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/039,315  
FILING DATE: 07-FEB-1997  
APPLICATION NUMBER: US 60/052,023  
FILING DATE: 09-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Zindrick, Thomas K.  
REGISTRATION NUMBER: 32,185  
REFERENCE/DOCKET NUMBER: A-430D  
INFORMATION FOR SEQ ID NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US 09 907 263-2  
Query Match 100.0%; Score 941; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2, 8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISCTCKHKTLYLNCQPGQDTCPECSGFTASENHLRHCL 60  
Db 1 DSVCPQGYIHPQNNISCTCKHKTLYLNCQPGQDTCPECSGFTASENHLRHCL 60  
QY 61 SCSCPKFEMQVEISSCTVDRDTGCGKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
Db 61 SCSCPKFEMQVEISSCTVDRDTGCGKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 121 KQNTVCTCHAGFFLEPNECVSNCNFKKSECTKLCLOPIEN 161

Db 121 KQNTVCTCHAGFFLEPNECVSNCNFKKSECTKLCLOPIEN 161

RESULT 6  
US-09-899-429A-6  
Sequence 6, Application US/0909429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
Himmeler, Adolph  
APPLICANT: Maurer-Foggy, Ingrid  
Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and TNF Binding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO: 6  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-PP sequence  
US-09-899-429A-6

Query Match 100.0%; Score 941; DB 9; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2, 8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSVCPQGYIHPQNNISCTCKHKTLYLNCQPGQDTCPECSGFTASENHLRHCL 60  
Db 2 DSVCPQGYIHPQNNISCTCKHKTLYLNCQPGQDTCPECSGFTASENHLRHCL 61  
QY 61 SCSCPKFEMQVEISSCTVDRDTGCGKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
Db 62 SCSCPKFEMQVEISSCTVDRDTGCGKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFFLEPNECVSNCNFKKSECTKLCLOPIEN 161  
Db 122 KQNTVCTCHAGFFLEPNECVSNCNFKKSECTKLCLOPIEN 162

RESULT 7  
US-09-798-789-9  
Sequence 9, Application US/09798789  
Patent No. US20020009780A1  
GENERAL INFORMATION:  
APPLICANT: Dahiyat, Bassil  
Filikov, Anton  
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF ALPHA  
TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
DISORDERS  
FILE REFERENCE: A-68990-1/RPT/RMS/BMZ  
CURRENT APPLICATION NUMBER: US/09/798,789  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: US 60/186,427  
PRIOR FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-798-789-9

Query Match 100.0%; Score 941; DB 10; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2, Re-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECSGSPFASENHLRHCL 60  
DB 2 DSVCPQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECSGSPFASENHLRHCL 61  
QY 61 SCSKREMGQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
DB 62 SCSKREMGQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFLPENEVCVSNCKSKLECTKLCIPQIEN 161  
DB 122 KQNTVCTCHAGFLPENEVCVSNCKSKLECTKLCIPQIEN 162

RESULT 8  
US-09-798-789-22  
Sequence 22, Application US/09798789  
Patent No. US2002009780A1  
GENERAL INFORMATION:  
APPLICANT: Dahiya, Basill  
APPLICANT: Filikov, Anton  
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA  
TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
FILE REFERENCE: A-68990-1/RET/RMS/EMK  
CURRENT APPLICATION NUMBER: US/09/798,789  
CURRENT FILING DATE: 2001-03-02  
PRIORITY FILING DATE: 2000-03-02  
PRIORITY FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-798-789-22

Query Match 100.0%; Score 941; DB 10; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2, Re-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECSGSPFASENHLRHCL 60  
DB 2 DSVCPQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECSGSPFASENHLRHCL 61  
QY 61 SCSKREMGQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
DB 62 SCSKREMGQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFLPENEVCVSNCKSKLECTKLCIPQIEN 161  
DB 122 KQNTVCTCHAGFLPENEVCVSNCKSKLECTKLCIPQIEN 162

RESULT 9  
US-09-899-429A-20  
Sequence 20, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph

APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-20

Query Match 100.0%; Score 941; DB 9; Length 172;  
Best Local Similarity 100.0%; Pred. No. 3e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECSGSPFASENHLRHCL 60  
DB 2 DSVCPQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECSGSPFASENHLRHCL 61  
QY 61 SCSKREMGQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 120  
DB 62 SCSKREMGQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCINGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFLPENEVCVSNCKSKLECTKLCIPQIEN 161  
DB 122 KQNTVCTCHAGFLPENEVCVSNCKSKLECTKLCIPQIEN 162

RESULT 10  
US-09-899-429A-16  
Sequence 16, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20

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; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US 09 899 429A 16

Query Match 100.0%; Score 941; DB 9; Length 173;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYHPQNNISCTCTKTKYLYNDCPGPGQDTDCPEESGFTASENHLPHCL 60
DB 13 DSVCPQGVYHPQNNISCTCTKTKYLYNDCPGPGQDTDCPEESGFTASENHLPHCL 72

QY 61 SCSKCRKEMGQVEISSCTVDPRTVCGPFPKQYRHYWSENLFCQCFNCSLCINGTVHLSQCF 120
DB 73 SCSKCRKEMGQVEISSCTVDPRTVCGPFPKQYRHYWSENLFCQCFNCSLCINGTVHLSQCF 132

QY 121 KQNTVCTCHAGFFLPENECVSCNCKKSELECTKLCLOPIEN 161
DB 133 KQNTVCTCHAGFFLPENECVSCNCKKSELECTKLCLOPIEN 173

RESULT 11
US-09-899-429A-10
; Sequence 10, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-18

Query Match 100.0%; Score 941; DB 9; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.2e-61;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYHPQNNISCTCTKTKYLYNDCPGPGQDTDCPEESGFTASENHLPHCL 60
DB 30 DSVCPQGVYHPQNNISCTCTKTKYLYNDCPGPGQDTDCPEESGFTASENHLPHCL 89

QY 61 SCSKCRKEMGQVEISSCTVDPRTVCGPFPKQYRHYWSENLFCQCFNCSLCINGTVHLSQCF 120
DB 90 SCSKCRKEMGQVEISSCTVDPRTVCGPFPKQYRHYWSENLFCQCFNCSLCINGTVHLSQCF 149

QY 121 KQNTVCTCHAGFFLPENECVSCNCKKSELECTKLCLOPIEN 161
DB 150 KQNTVCTCHAGFFLPENECVSCNCKKSELECTKLCLOPIEN 190

RESULT 13
US-09-899-429A-12
; Sequence 12, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
```









A.Residues: 1-455 <GRA>  
A.Cross-references: GB:M3764  
A.Note: The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372Z  
R.Neubart, Y., Kempfer, O., Birkenbusch, C., Engelmann, H., Zwarg, R., Adenka, Z., Heilmann,  
EMBO J. 9, 3269-3278, 1990  
Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the TNF  
le form of the receptor.  
A.Reference number: S12057, MUID:91006021, PMID:1698610  
A.Accession: S12057  
A.Molecule type: mRNA  
A.Residues: 1-455 <NOB>  
A.Cross-references: EMBL:X55113, NID:937223, PIDN:CA93021.1, PID:937224  
A.Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
Gene 134, 209-216, 1993  
P.Kemper, O.; Wallach, D.  
Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A.Reference number: J10758, MUID:94085779, PMID:826379  
A.Accession: J10758  
A.Molecule type: DNA  
A.Residues: 1-13 <KEM>  
P.Scheininger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A.Reference number: AC0231, MUID:90292216, PMID:2113477  
A.Accession: AC0231  
A.Molecule type: protein  
A.Residues: 41-43,'X','45-53,'X','55-57 <SEC>  
R.Garganana, T., Huang, C., Kohr, W., Cappuccini, F., Lucchi III, J.A., Jeffes, E.W.B., Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
Title: Purification and characterization of an inhibitor (soluble tumor necrosis fact  
clients.  
A.Reference number: A39258, MUID:91062364, PMID:2174164  
A.Accession: A39258  
A.Molecule type: protein  
A.Residues: 41-60 <GAP>  
A.Experimental source: cancer patient serum  
R.Olsson, I., Larre, M., Nilsson, E., Peetre, C., Thyrell, H., Grubb, A., Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
Title: Isolation and characterization of a tumor necrosis factor binding protein from  
A.Reference number: AC0594, MUID:89171156, PMID:2324890  
A.Accession: AC0594  
A.Molecule type: protein  
A.Residues: 41-43,'X','45-53,'V','55-57,'XK',60 <OLS>  
A.Experimental source: renal failure patient urine  
E.Engelmann, H., Thewissen, D., Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A.Reference number: A15010, MUID:90110215, PMID 2153136  
A.Accession: A15010  
A.Molecule type: protein  
A.Residues: 41-45 <ENG>  
A.Experimental source: normal urine  
P.Kihara, J., Asada, A., Kihara, S., Kato, K  
Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994  
Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
A.Reference number: J02404, MUID:95128033, PMID:7765720  
A.Accession: J02404  
A.Molecule type: protein  
A.Residues: 41'53,'X','55-144,'X','146-150,'X','152-186,'X','188-201 <KAU>  
A.Experimental source: urine  
C.Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
Genetics:  
A.Gene: GDB:TNFR1  
A.Cross-references: CDB:125913, OMIM:191190  
A.Map position: 1p33.2-1p33.2  
A.Introns: 13/3, 65/1, 108/1, 158/1, 184/2, 209/1, 247/1, 256/3, 353/1  
C\_SUPERfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C\_KEYWORDS: duplication, glycoprotein, receptor, transmembrane protein  
F1-21/DOMAIN: signal sequence #status predicted <SIG>  
F22-455/Product: tumor necrosis factor receptor 1 #status predicted <EXT>  
F33-211/DOMAIN: extracellular #status predicted <EXT>  
F44-201/Product: TNF binding protein 1 [tumor necrosis factor alpha inhibitor] #status  
F44-82/DOMAIN: NGF receptor repeat homology <NGI>

F.84-126/Domain: NGF receptor repeat homology <NG2>  
 F.127-167/Domain: NGF receptor repeat homology <NG3>  
 F.168-196/Domain: NGF receptor repeat homology <NG4>  
 F.212-234/Domain: transmembrane #status predicted <MEM>  
 F.235-455/Domain: intracellular #status predicted <INT>  
 F.54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 8,3e-62; Indels 0; Gaps 0;  
 Matches 161, Conservative 0; Mismatches 0;

QY 1 DSVCPQGYIHPNNISICTCKCHKGTLYLNDPCPGQDTRCECGSFTASENHLRHCL 60  
 Db 41 DSVCPQGYIHPNNISICTCKCHKGTLYLNDPCPGQDTRCECGSFTASENHLRHCL 100  
 |||  
 QY 61 SCSCRKEMQVVEISCTYDRDPTVCGCRKNQRYRHWSNLFQPCNGSLCLNGTVHLSCQE 120  
 Db 101 SCSCRKEMQVVEISCTYDRDPTVCGCRKNQRYRHWSNLFQPCNGSLCLNGTVHLSCQE 160  
 |||  
 QY 121 KQNTVCTCHAGFFLRENECVSCSNCKSLLECTKCLPDIEN 161  
 Db 161 KQNTVCTCHAGFFLRENECVSCSNCKSLLECTKCLPDIEN 201  
 |||

RESULT 2  
 JC4302  
 tumor necrosis factor receptor p55 precursor - pig  
 C.Species: Sus scrofa domestica (domestic pig)  
 C.Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
 C.Accession: J04302; PC4093  
 R.Steier, B., Pauli, U.  
 Gene 163, 263 266, 1995  
 A.Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor  
 A.Reference number: JC4302; PMID:7590278  
 A.Accession: J04302  
 A.Molecule type: mRNA  
 A.Residues: 1-461 <SUT>  
 A.Cross-references: GB:U19994, NID:g1141752, PIDN:AAC8499.1, FID:g1141753  
 A.Accession: PC4093  
 A.Molecule type: protein  
 A.Residues: 1-7 <SUT>  
 A.Experimental source: kidney cell line 15  
 C.Genetics:

A:Gene: tnfr  
 C:Superfamily: tumor necrosis factor receptor type 1, NGF receptor repeat homology  
 C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
 F.1-29/Domain: signal sequence #status predicted <SIG>  
 F.30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
 F.44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
 F.44-82/Domain: NGF receptor repeat homology <NG1>  
 F.84-126/Domain: NGF receptor repeat homology <NGF>  
 F.211-231/Domain: transmembrane #status predicted <TM>  
 F.235-455/Domain: intracellular #status predicted <INT>  
 F.54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 716.5; DB 2; Length 461;  
 Best Local Similarity 77.4%; Pred. No. 2e-45; Indels 1; Gaps 1,  
 Matches 120, Conservative 12; Mismatches 22;

QY 1 DSVCPQGYIHPNNISICTCKCHKGTLYLNDPCPGQDTRCECGSFTASENHLRHCL 60  
 Db 41 DSVCPQGYIHPNNISICTCKCHKGTLYLNDPCPGQDTRCECGSFTASENHLRHCL 100  
 |||  
 QY 61 SCSCRKEMQVVEISCTYDRDPTVCGCRKNQRYRHWSNLFQPCNGSLCLNGTVHLSCQE 120  
 Db 101 SCSCRKEMQVVEISCTYDRDPTVCGCRKNQRYRHWSNLFQPCNGSLCLNGTVHLSCQE 160  
 |||  
 QY 121 KQNTVCTCHAGFFLRENECVSCSNCKSLLECTKCL 155  
 Db 161 KQNTVCTCHAGFFLRENECVSCSNCKSLLECTKCL 194

RESULT 3





A:Reference number: 154182; MUID:93252381; PMID:8486360  
 A:Accession: 154182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <RES>  
 A:Cross-references: GB:L04270; NID:9339761; PIR:AAA36757.1; PID:9339762  
 C:Genetics:  
 A:Gene: GDB:LTBR  
 A:Cross-references: GDB:1230195; OMIM:600979  
 A:Map position: 17q21.31-32  
 A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 19.9%; Score 187.5; DB 2; Length 435;  
 Best Local Similarity 32.7%; Pred. No. 7.4e-07;  
 Matches 49; Conservative 17; Mismatches 71; Indels 13; Gaps 7;

QY 8 FYHFNANSICCTKCKKGYLYNDGPGDDTDCREC-ESGSFTASENHLRLCLSC 67  
 DB 49 EYEPQHR-ICCSRCPEPTYSAK-SRIPTVCATCAENYNHMYLTICQLCRCPD 106  
 C: 68 EWGVETSSCTVPEPTVCCDEPNVYHWSNLPQPCNCS-CLNGVHLSCQE-KQ 122  
 DB 107 VMLEELHACTSKRTQCRQCPMFCAMAA--LECHCELLSDCPPTAEKLDEVGKG 163  
 QY 123 NTVCCT-CHAGFPFLRE-NECVSGSNC---KSLCTK 153  
 DB 164 NMHCVPCTAGH--QNTSSPSARCPHTRC 191

RESULT 6  
 GCHUN  
 nerve growth factor receptor precursor, low affinity [validated] - human  
 N:Alternate names: NGF receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1988 #sequence, revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C:Accession: A05218; A60204; S21687; 157638  
 P:Johnson, D.; Latham, A.; Ruck, C.P.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
 Cell 47, 545-554, 1986  
 A:Title: Expression and structure of the human NGF receptor.  
 A:Reference number: A05218; MUID:8708725; PMID:3022937  
 A:Accession: A05218  
 A:Molecule type: mRNA  
 A:Residues: 1-427 <JOB>  
 A:Cross-references: GB:M4764; NID:9189204; PIR:AA59544.1; PID:9189205  
 P:Marano, N.; Dierschold, B.; Earley Jr., J.J.; Schaltenman, G.; Thompson, S.; Grob, P.;  
 J. Neurochem. 48, 225-233, 1987  
 A:Title: Purification and amino terminal sequencing of human melanoma nerve growth facto  
 A:Reference number: A60204; MUID:8708574; PMID:3025363  
 A:Accession: A60204  
 A:Molecule type: Protein  
 A:Residues: 29, 31, 33, 42, 44, 45, 46, 47, 50-51, 54-56 <MAR>  
 A:Experimental source: melanoma cell line A875  
 A:Note: this sequence has been corrected by a note added in proof to follow the nucleoti  
 R.Vissavajjalal, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
 Arch. Biochem. Biophys. 234, 244-252, 1992  
 A:Title: Structural domains of the extracellular domain of human nerve growth factor rec  
 A:Reference number: S21689; MUID:92198017; PMID:1372492  
 A:Accession: S21689  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 183-208 <VIS>  
 R:Sehgal, A.; Patil, N.; Chao, M.  
 Mol. Cell. Biol. 8, 3160-3167, 1988  
 A:Title: A constitutive promoter directs expression of the nerve growth factor receptor  
 A:Reference number: 157638; MUID:89096903; PMID:2850481  
 A:Accession: 157638  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:Cross-references: GB:M1621; NID:9189206; PIR:AA36363.1; PID:9189207  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w

C:Comment: This receptor undergoes both N- and O-linked glycosylation.  
 C:Genetics:  
 A:Gene: GDB:NGFR  
 A:Cross-references: GDB:120234; OMIM:162010  
 A:Map position: 17q21.17q22  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F.1-28/Domain: signal sequence #status predicted <SIG>  
 F.29-427/Product: nerve growth factor receptor #status experimental <MAT>  
 F.29-250/Domain: extracellular #status predicted <EXT>  
 F.32-65/Domain: NGF receptor repeat homology <NG1>  
 F.67-108/Domain: NGF receptor repeat homology <NG2>  
 F.109-147/Domain: NGF receptor repeat homology <NG3>  
 F.149-189/Domain: NGF receptor repeat homology <NG4>  
 F.197-248/Region: serine/threonine-rich  
 F.251-272/Domain: transmembrane #status predicted <TRM>  
 F.273-447/Domain: intracellular #status predicted <INT>  
 F.60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 182.5; DB 1; Length 427;  
 Best Local Similarity 32.1%; Pred. No. 1.7e-06;  
 Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11;

QY 4 CPOGYIHPQNNISICTKCKKGYLYNDGPGDDTDCREC-ESGSFTASENHLRLCLSC 62  
 DB 32 CPTGLYTH---SGECCACNLGEGVAQC-GANQ-TVCEPCLDSTVSQVATPECKPC 86  
 QY 63 SKCRKMGQVEIIS-CTVDRDTVCGRKQRYHWSNLPQPCNCSCLNGT-VHLSCQE 120  
 DB 87 TEC---VQLGSMSPACVEADDAVCRG---AYGYQDETTRGCRACVCEAGSLVFSSCD 140

QY 121 KONTVC-TCHAGFPFLRE-NECVSGSNC---KSLCTK 153  
 DB 141 KONTVCBCPDGYTSDAHNVDPCLPTVCEDTERQLRECTR 182

RESULT 7  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence, revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 P:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r  
 A:Reference number: A38634; MUID:91187885; PMID:1845278  
 A:Accession: A38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:9199827; PIR:AAA39752.1; PID:9199828  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Bradman, C.T.; Copeland, N.G.; Jenk  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A:Reference number: A40254; MUID:91246168; PMID:1645445  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:9199827; PIR:AAA39752.1; PID:9199828  
 R:Kisilevich, M.; Fallowes, R.; Feldmann, M.; Chetnaiovsky, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
 A:Reference number: S54816  
 A:Accession: S54816  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KIS>  
 A:Cross-references: EMBL:X87128; NID:9809043; PIR:CAA60618.1; PID:9809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F.1-32/Domain: signal sequence #status predicted <SIG>  
 F.32-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F.470-777/Domain: NGF receptor repeat homology <NG1>  
 F.79-120/Domain: NGF receptor repeat homology <NG2>

F:166 201/Domain: NGF receptor repeat homology <NG>  
 Query Match 19.2% Score 181; DB 2; Length 474;  
 Best Local Similarity 31.7% Pred No 2 3e-06;  
 Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;  
 QY 4 CPGKYYIHPPNNISICTYCHKGTLYNDPCPGQDTCPECSGFTASENHLPCHLSC 62  
 DB 40 COISQRYVDRKACMCAPPPGVYVHFC-NKTSDTVCADCEASMYTCVMNQPFCLSCS 98  
 QY 61 SKCPVEMQVEISSCTVPRDVTCCGPKNOY-----PHYSENLPFCNCLSLNG-TVHLS 117  
 DB 99 SSTTTH--QVEIPATCKQNNPVA'EAGPYCALKTH--SGSCPCMLPSVPGPGFVASS 154  
 QY 118 CGEKONTV--TCHAGFFLPENECVSCNCKSECTKLTLP 157  
 DB 155 RAPNENVLCKACAPTF--SDTTSSTVCPHPICSLAIP 193  
 RESULT R  
 T2 protein - myxoma virus (strain Lausanne)  
 C:Species: myxoma virus  
 C>Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
 C:Accession: A40566  
 R:Upton, C.; Macen, J. L.; Schreiber, M.; McFadden, G.  
 Virology 184, 370-382, 1991  
 A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor  
 A:Reference number: A40566; MUID:91335768; PMID:1651597  
 A:Accession: A40566  
 A:Molecule type: DNA  
 A:Residues: 1-326 <UPT>  
 A:Cross references: GB:M05181; GR:M37376; RID:3332302; PID:AAA46612 1; PID g332310  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 C:Keywords: glycoprotein  
 F:64.105/Domain: NGF receptor repeat homology <NG2>  
 F:106.147/Domain: NGF receptor repeat homology <NG>  
 F:66.181.205.248/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 19.1% Score 179.5; DB 1; Length 326;  
 Best Local Similarity 27.4% Pred No 2 3e-06;  
 Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7;  
 QY 13 QNNSICTYCHKGTLYNDPCPGQDTCPECSGFTASENHLPCHLSC-SKCRKEMGQ 71  
 DB 34 EKDHCTCTCPSPSVASPLC-GPGSDTVCSPCKNETFTASTNHAPACVSCRCGRCTGHL 91  
 QY 72 VEISSCTVPRDVTCCGPKNOY-----PHYSENLPFCNCLSLNG-TVHLS 117  
 DB 92 ESQCDTRDVPVCHSACNYCLLGGQGGPICAPFTYCPAGYGVSGHTPTGDVLCTKCP 150  
 QY 93 RHVWENLPQCFNCLSLNG-TVHLSQCFKQNTVCTCHAGFFLPENECVSCNCKSLEC 151  
 DB 151 RVTYSDAVSTSTCTCTSSNYISVERNLVPVNDTCTTTAG----PNEVKTSEFSVTLNH 206  
 QY 152 TKLCLP 157  
 DB 207 TD-CBP 211  
 RESULT 9  
 B41692  
 T2 protein rabbit fibroma virus  
 C:Species: rabbit fibroma virus, Shope fibroma virus  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: B41692  
 R:Upton, C.; Detlange, A. M.; McFadden, G.  
 Virology 160, 20-30, 1987  
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
 A:Reference number: A43692; MUID:87321103; PMID:2826128  
 A:Accession: B41692  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-325 <UPT>  
 A:Cross references: GB:M17433  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:64.105/Domain: NGF receptor repeat homology <NG2>  
 F:106.147/Domain: NGF receptor repeat homology <NG3>  
 Query Match 18.0% Score 178; DB 2; Length 325;  
 Best Local Similarity 29.6% Pred No 3e-06;  
 Matches 45; Conservative 15; Mismatches 62; Indels 40; Gaps 6;  
 QY 13 QNNSICTYCHKGTLYNDPCPGQDTCPECSGFTASENHLPCHLSC-SKCRKEMGQ 71  
 DB 34 EKDHCTCTCPSPSVASPLC-GPGSDTVCSPCKNETFTASTNHAPACVSCRCGRCTGHL 91  
 QY 72 VEISSCTVPRDVTCCGPKNOYPHYSENLPFCNCLSLNG-TVHLS 117  
 DB 92 ESQCDTRDVPVCHSACNYCLLGGQGGPICAPFTYCPAGYGVSGHTPTGDVLCTKCP 150  
 QY 132 FFLRENECVSCNCK-----SLECTKLC 155  
 DB 133 YGVSGHTPRADTLCCKPPHTYSNLSLSTPTEFC 164  
 RESULT 10  
 A26431  
 nerve growth factor receptor precursor, low affinity - rat  
 N:Alternate names: NGF receptor  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A26431; PH1229  
 R:Radeke, M. J.; Misko, T. F.; Hsu, C.; Herzenberg, L. A.; Shooter, E. M.  
 Nature 325, 593-597, 1987  
 A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor  
 A:Reference number: A26431; MUID:87115859; PMID:3027580  
 A:Accession: A26431  
 A:Molecule type: mRNA  
 A:Residues: 1-425 <RAD>  
 A:Cross references: GB:X05137; RID:g56755; PID:CAA28781.1; PID:0466766  
 R:Metsis, M.; Timusk, T.; Allikmets, R.; Saarma, M.; Persson, H.  
 Gene 121, 247-254, 1992  
 A:Title: Regulatory elements and transcriptional regulation by testis-specific and retinoblastoma  
 A:Reference number: PH1229; MUID:93077038; PMID:1446821  
 A:Accession: PH1229  
 A:Molecule type: DNA  
 A:Residues: 1-20 <MET>  
 A:Cross references: GB:X61269  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells  
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of the  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates with  
 C:Genetics:  
 A:Introns: 20/3  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphorylation; receptor;  
 F:1.29/Domain: signal sequence #status predicted <SIG>  
 F:30-425/Product: nerve growth factor receptor #status predicted <EXT>  
 F:30-251/Domain: extracellular #status predicted <EXT>  
 F:33-66/Domain: NGF receptor repeat homology <NG1>  
 F:68-109/Domain: NGF receptor repeat homology <NG2>  
 F:110-148/Domain: NGF receptor repeat homology <NG3>  
 F:150-190/Domain: NGF receptor repeat homology <NG4>  
 F:198-249/Region: serine/threonine-rich  
 F:252-273/Domain: transmembrane #status predicted <MEM>  
 F:274-425/Domain: intracellular #status predicted <INT>  
 F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 18.8% Score 176.5; DB 1; Length 425;  
 Best Local Similarity 30.9% Pred No 4 6e-06;  
 Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 19;  
 QY 4 CPGKYYIHPPNNISICTYCHKGTLYNDPCPGQDTCPECSGFTASENHLPCHLSC 62  
 DB 33 CSTGLYTH---SGECCVACNLGEGVAQPC-GANG-TVCEPCLDNVTSIDVVSATETCTCC 87



A:Cross references: EMBL:L22579; MID:g623595; PIDN:AAA60033.1; PID:g419102  
A:Experimental source: strain Bangladesh 1975  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17 4%; Score 164; DB 2; Length 348;  
Best Local Similarity 27.8%; Pred. No. 3.3e-05;  
Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

QY 4 CPOKHYIHPQNNISICTCHKCTYLYNCPGPGQDTDCRECSGFTASFNHLPACLSLCS 63  
DB 41 CKDTEY---KPHNLCCISCPCTVASPLCDSK-TNTQCTPGSGTFTSRNNHLPACLSLN 86  
QY 64 KQKFMQVEISSCTVDPDTVCGGPKNQPHYWSENLFQCF...NCSLCLNGTVHLS 117  
DB 87 GRGNS--NQVETFSCTTHNRIICECPGY-----CLLKSGSGCKACVST---- 130

QY 118 CQEKQNTVCTCHAGFFLENECVS---CSNC 145

DB 131 -----KCGIGYGVSGHTSVGDVICSPC 152

## RESULT 15

D36858

Gene G4R protein - variola virus

N:Alternate names: B2BR protein (COP)

C:Species: variola virus

C&gt;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text\_change 23-Mar-2001

C:Accession: D36858; S46888; S32385; S35987

R:Blinov, V.M.

submitted to GenBank, November 1992

A:Reference number: A16859

A:Accession: D36858

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 &lt;BL&gt;

A:Cross references: GB:X69198; MID:g456758; PIDN:CAA49137.1; PID:g457087

A:Experimental source: strain India-1967, ssp. major, isolate Ind3

R:Kolykhailov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Prok

submitted to the EMBL Data Library, April 1992

A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P

A:Reference number: S46888

A:Accession: S46888

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 &lt;KOL&gt;

A:Cross references: EMBL:X67117; MID:g516428; PIDN:CAA47540.1; PID:g516449

A:Experimental source: strain India-1967, isolate Ind3

R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.

PERS Lett. 319, 80-83, 1993

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A:Reference number: S32385; MID:g1262241; PID:81941.3

A:Accession: S32385

A:Molecule type: DNA

A:Residues: 31-168 &lt;SHC&gt;

A:Cross references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major

C:Genetics:

A:Gene: G4R

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F:32 66/Domain: NGF receptor repeat homology &lt;NGF&gt;

F:68 109/Domain: NGF receptor repeat homology &lt;NG2&gt;

F:110 151/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match

Best Local Similarity 17.4%; Score 164; DB 2; Length 349;

Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

QY 4 CPOKHYIHPQNNISICTCHKCTYLYNCPGPGQDTDCRECSGFTASFNHLPACLSLCS 63

DB 42 CKDTEY---KPHNLCCISCPCTVASPLCDSK-TNTQCTPGSGTFTSRNNHLPACLSLN 87

QY 64 KQKFMQVEISSCTVDPDTVCGGPKNQPHYWSENLFQCF...NCSLCLNGTVHLS 117



GenCore version 5.1.3  
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CM protein - protein search, using sw model

Run on: January 6, 2003, 03:46:34 ; Search time 14 Seconds  
(without alignments)

476.978 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQKQYHPQNNISCTT... CSNCFYSLECTKLCPLQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	455	1	TR1A_HUMAN
2	716.5	76.1	461	1	TR1A_PIG
3	680	72.3	454	1	TR1A_MOUSE
4	674.5	71.7	471	1	TR1A_BOVIN
5	669	71.1	461	1	TR1A_RAT
6	200.5	21.3	176	1	TR23_MOUSE
7	200.5	21.3	417	1	TR12_HUMAN
8	198.5	21.1	180	1	TR22_MOUSE
9	187.5	19.9	435	1	TRN3_HUMAN
10	182.5	19.4	427	1	TR16_HUMAN
11	181.5	19.3	417	1	TR16_MOUSE
12	181	19.2	474	1	TR1B_MOUSE
13	179.5	19.1	326	1	V72_MXVL
14	178	18.9	325	1	V72_SFVKA
15	176.5	18.8	332	1	TRN6_PIG
16	176.5	18.8	425	1	TR16_RAT
17	167.5	17.8	249	1	TRN5_MOUSE
18	167.5	17.8	415	1	TRN3_MOUSE
19	167	17.7	269	1	TRN5_BOVIN
20	166.5	17.7	323	1	TRN6_BOVIN
21	166.5	17.7	349	1	TRN6_CAMPES
22	164	17.4	349	1	TRN6_VARV
23	164	17.4	351	1	TRN6_CAMPX
24	164	17.4	401	1	TR1R_HUMAN
25	162.5	17.3	327	1	TRN6_MOUSE
26	161	17.1	461	1	TR1B_HUMAN
27	158	16.8	401	1	TR1B_RAT
28	154	16.4	401	1	TR1B_MOUSE
29	147	15.6	324	1	TRN6_RAT
30	147	15.4	416	1	TR16_CHICK
31	142	15.1	283	1	TR14_HUMAN
32	142	15.1	386	1	TR10D_HUMAN
33	141	15.0	1680	1	FUR2_DROME

RESULT 1

ID	TR1A_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor binding protein 1 (TBP1)]			
GN	TNFRSF1A OR TNFR1 OR TNFAR.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Leniz P., Paab H., Kohr W.J., Goeddel D.V.			
RA	"Molecular cloning and expression of a receptor for human tumor necrosis factor."			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tabuchi H., Lesslauer W.			
RA	"Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor."			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 41-53, 110 124 AND 199 201.			
RX	MEDLINE=91006021; PubMed=1698610;			
RA	Nopar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R., Aderka D., Holtmann H., Wallach D.			
RA	"Soluble forms of tumor necrosis factor receptors (TNF-R). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor."			
RL	EMBO J. 9:3263-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Foy I., Kronke M., Scheurich P., Pflizenmaier K., Lantz M., Glisson I., Hauptmann R., Strataw C., Adolf G.R.			
RA	"Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein."			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Placenta;			
RC	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			

P41272 mus musculus  
P25942 homo sapiens  
G14798 h tumor nec  
P26842 homo sapien  
G14763 homo sapien  
Q08115 Erythrocytes  
Q04592 mus musculus  
P92127 gliadina 14m  
Q92045 mus musculus  
Q92824 homo sapien  
P47741 mus musculus  
P25445 homo sapien

CC "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
 CC expression of recombinant soluble TNF-binding protein.",  
 CC Proc Natl Acad Sci U S A. 87:7380-7384(1990).  
 CC [6].  
 CC RX MEDLINE=92250049; PubMed=115171;  
 CC Fuchs F., Stehl S., Dworzak M., Himmler A., Ambros P.F.;  
 CC "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
 CC localization to chromosome 12p13.";  
 CC Genomics 12:220-224(1992).  
 CC [7].  
 CC RX SEQUENCE FROM N.A.  
 CC TISSUE=Muscle;  
 CC Strausberg R.;  
 CC Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC [8].  
 CC RX SEQUENCE OF 41-45; PubMed=2153136;  
 CC Engelmann H., Novick D., Wallach D.;  
 CC "Two tumor necrosis factor-binding proteins purified from human  
 CC urine. Evidence for immunological cross-reactivity with cell surface  
 CC tumor necrosis factor receptors.";  
 CC J. Biol. Chem. 265:1531-1536(1990).  
 CC [9].  
 CC RX X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
 CC MEDLINE=93258809; PubMed=8387891;  
 CC Bacher P.W., P'Avry A., Jones W., Schoenfeld H.-C.,  
 CC Bioger C., Loetscher H., Lesslauer W.;  
 CC "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 CC beta complex: implications for TNF receptor activation.";  
 CC Cell 73:431-445(1993).  
 CC [10].  
 CC RX X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 CC MEDLINE=97094982; PubMed=8939750;  
 CC Nalsmith J.H., Devine T.G., Khoo H., Sprang S.R.;  
 CC "Structures of the extracellular domain of the type I tumor necrosis  
 CC factor receptor.";  
 CC Structure 4:1251-1262(1996).  
 CC [11].  
 CC RX VARIANT: ENF ASG-59, TYR-62, MET-79, PHE-81, ARG-117 AND TYR-117.  
 CC MEDLINE=94213501; PubMed=10194207;  
 CC McDermott M.F., Aksevitjevich I., Galon J., McDermott E.M.,  
 CC Ogunkolade B.W., Gentaola M., Mansfield E., Gattin M., Korosyan L.,  
 CC Petersson T., McCarthy J., Frucht D.M., Aringer M., Terosyan Y.,  
 CC Teppo A.-M., Wilson M., Karastan H.M., Man Y., Todd I., Wood G.,  
 CC Scolding P., Kuzajewa T.P., Cooper S.M., Vella R.P., Amos C.I.,  
 CC Mulley G.A., O'Shea J., Kastner D.L.;  
 CC "Germane mutations in the extracellular domains of the 55 kDa TNF  
 CC receptor, TNFR1, define a family of dominantly inherited  
 CC autoinflammatory syndromes.";  
 CC Cell 97:133-144(1999).  
 CC [12].  
 CC RX FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activating receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis. Contributes to  
 CC the induction of noncytotoxic TNF effects including anti-viral  
 CC state and activation of the acid sphingomyelinase.  
 CC [13].  
 CC RX SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC [14].  
 CC RX SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC [15].  
 CC RX DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC [16].  
 CC RX PTM: The soluble form is produced from the membrane form by  
 CC proteolytic processing.  
 CC [17].  
 CC RX DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
 CC familial hibernian fever (PHF), a disease characterized by  
 CC recurrent fever, abdominal pain, localized tender skin lesions and  
 CC myalgia.  
 CC [18].  
 CC RX SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC [19].  
 CC RX SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC [20].  
 CC RX DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".  
 CC [21].  
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 CC [22].  
 CC RX EMBL; X55313; CAA39021.1; -;  
 CC EMBL; M33294; AAA03210.1; -;  
 CC EMBL; M58286; AAA36753.1; -;  
 CC EMBL; M63121; AAA36754.1; -;  
 CC EMBL; M75866; AAA61201.1; -;  
 CC EMBL; M75864; AAA61201.1; JOINED.  
 CC EMBL; M75865; AAA61201.1; JOINED.  
 CC EMBL; M60275; AAA36756.1; -;  
 CC EMBL; A21522; CAA01558.1; -;  
 CC EMBL; BC010140; AAH01040.1; -;  
 CC PIR; A34899; GQHUTL.  
 CC PIR; A35010; A35010.  
 CC PIR; S12057; S12057.  
 CC PIR; A38208; A38208.  
 CC PDB; 1TNR; 31-JUL-94.  
 CC PDB; 1NCF; 07-DEC-95.  
 CC PDB; 1EXT; 11-JAN-97.  
 CC GeneW; HGNC:11916; TNFRSF1A.  
 CC MIM; 191190; -;  
 CC MIM; 142680; -;  
 CC InterPro; IPR000488; Death.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF000320; TNFR\_c6; 4.  
 CC Pfam; PF005311; death; 1.  
 CC ProDom; PD000771; TNFR\_c6; 1.  
 CC SMART; SM00005; DEATH; 1.  
 CC SMART; SM00308; TNFR; 4.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 CC PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 CC PROSITE; PS50017; DEATH DOMAIN; 1.  
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
 CC Disease mutation; Polymorphism; 3d-structure.  
 CC SIGNAL  
 CC FT 1 21  
 CC FT CHAIN 22 455  
 CC FT  
 CC FT CHAIN 41 291  
 CC FT DOMAIN 22 211  
 CC FT DOMAIN 212 234  
 CC FT DOMAIN 235 455  
 CC FT REPEAT 43 82  
 CC FT REPEAT 83 125  
 CC FT REPEAT 126 166  
 CC FT REPEAT 167 196  
 CC FT DOMAIN 338 348  
 CC FT DOMAIN 356 441  
 CC FT DISULFID 44 58  
 CC FT DISULFID 59 72  
 CC FT DISULFID 62 81  
 CC FT DISULFID 84 99  
 CC FT DISULFID 102 117  
 CC FT DISULFID 105 125  
 CC FT DISULFID 127 143  
 CC FT DISULFID 146 158  
 CC FT DISULFID 149 166  
 CC FT DISULFID 168 179  
 CC  
 CC TUMOR NECROSIS FACTOR RECEPTOR  
 CC SUPERFAMILY MEMBER 1A, MEMBRANE FORM.  
 CC TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC POTENTIAL.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TNFR-CYS 1.  
 CC TNFR-CYS 2.  
 CC TNFR-CYS 3.  
 CC TNFR-CYS 4.  
 CC N-SMASE ACTIVATION DOMAIN (NSD).  
 CC DEATH.



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Query Match 100 n% Score 941; DR 1; Length 455;
Best Local Similarity 100 n%; Pred No. 1 2e-71;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTPQGYTHPQNNISCTCTCHGCTVLYNDGPGPGQDTCPCECSGSPFASENHLRHCL 60
Db 41 DSVCPQGYTHPQNNISCTCTCHGCTVLYNDGPGPGQDTCPCECSGSPFASENHLRHCL 100

QY 61 SCSPCPPEMGEVEISSCTTVPDVTGCPQYHYWSENLCGPNCSLCINGTVHLSQCE 120
Db 101 SCSPCPPEMGEVEISSCTTVPDVTGCPQYHYWSENLCGPNCSLCINGTVHLSQCE 160

QY 121 KONTVCTCHAGFPLEPNCVSCNCFYSLETLCLPQIEN 161
Db 161 KONTVCTCHAGFPLEPNCVSCNCFYSLETLCLPQIEN 261

RESULT 2
TRIA FIG
ID TRIA FIG STANDARD; PRT; 461 AA.
AC P50555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina, Suidae, Sus.
OX NCBI TaxID=9823;
RN 1
RP SEQUENCE FROM N A
RC TISSUE=Kidney;
RX MEDLINE=96011645; PubMed=7590278;
RA Suter B., Pauli U.H.;
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT receptor."
RL Gene 163:263-266(1995).
CC 1- FUNCTION: Receptor for TNFRSF2/TNF alpha and homotrimeric
CC TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (by similarity).
CC SURINITE: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC 1- SURCELLULAR LOCATION: Type I membrane protein.
CC 1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC 1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC or send an email to license@sib-sib.ch)
CC
CC EMRL; U19994; AAC48499.1;
CC HSSP; P19438; 1TNR.
CC InterPro; IPR000488; Death.
CC Pfam; PF00020; TNFR_C6; 3.
CC Pfam; PF00531; Death; 1
CC ProDom; PD000771; TNFR_C6; 1.
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DR SMART; SM00005; DEATH; 1.
DP SMART; SM00208; TNFR; 3.
DP PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
PW Receptor; Apoptosis; Transmembrane; glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 1A.
FT DOMAIN 22 230 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 233 POTENTIAL.
FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 195 TNFR-CYS 4.
FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NCSD).
FT DEATH 362 447 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 194 BY SIMILARITY.
FT DISULFID 185 190 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLNAC) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLNAC) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLNAC) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLNAC) (POTENTIAL).
SQ SEQUENCE 461 AA; 50696 MW; 76118; Score 716.5; DR 1; Length 461;
Query Match 76.1%; Score 716.5; DR 1; Length 461;
Best Local Similarity 77.4%; Pred. No. 5.8e-53;
Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 DSVTPQGYTHPQNNISCTCTCHGCTVLYNDGPGPGQDTCPCECSGSPFASENHLRHCL 60
Db 41 ESLCPQGYTHPQNNISCTCTCHGCTVLYNDGPGPGQDTCPCECSGSPFASENHLRHCL 100

QY 61 SCSPCPPEMGEVEISSCTTVPDVTGCPQYHYWSENLCGPNCSLCINGTVHLSQCE 120
Db 101 SCSPCPPEMGEVEISSCTTVPDVTGCPQYHYWSENLCGPNCSLCINGTVHLSQCE 160

QY 121 KONTVCTCHAGFPLEPNCVSCNCFYSLETLCLPQIEN 155
Db 161 KONTVCTCHAGFPLEPNCVSCNCFYSLETLCLPQIEN 261

RESULT 3
TRIA_MOUSE
ID TRIA_MOUSE STANDARD; PPT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN 1
RP SEQUENCE FROM N A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
PA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
```

RT Necrosis factor receptors demonstrate one receptor is species specific.";  
 RL Proc Natl Acad Sci U S A 89:2830-2834(1991)  
 RL (2)  
 PP SEQUENCE FROM N A  
 EX MEDLINE=3:246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Cepeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor";  
 RL Mol Cell Biol 11:3020-3026(1991)  
 RN (3)  
 PP SEQUENCE FROM N A  
 EX MEDLINE=9:285014; PubMed=1647956;  
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,  
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;  
 RT "Cloning, expression and cross-linking analysis of the murine p55  
 RT tumor necrosis factor receptor";  
 RL Eur J Immunol 21:1649-1656(1991)  
 RN (4)  
 PP SEQUENCE FROM N A  
 RC TISSUE=Spleen;  
 RX MEDLINE=5:335815; PubMed=1657762;  
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b";  
 RL Immunogenetics 34:338-340(1991)  
 RN (5)  
 PP SEQUENCE FROM N A  
 EX MEDLINE=34:24292; PubMed 9188324,  
 RA Bebb B.F., Linthicum D.S.;  
 RT "Molecular sequence of the Tnf type 1 receptor from a mouse  
 RT endothelioma cell line";  
 RL Immunogenetics 39:450-451(1994)  
 RN (6)  
 PP SEQUENCE FROM N A  
 RX MEDLINE=33:3722; PubMed=8381516;  
 RA Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 RT "Genetic organization and promoter function of the murine tumor  
 RT necrosis factor receptor beta gene";  
 RL Mol Immunol 30:165-175(1993)  
 RN (7)  
 PP SEQUENCE FROM N A  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotypic  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (by similarity).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HEMAGGLUTINATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH CYST. REPEATS.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS. REPEATS.  
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 CC -----  
 DR EMBL; M59466; AAA39751.1; -;  
 DR EMBL; M59177; AAA40464.1; -;  
 DR EMBL; X57218; CAA41922.1; -;

DR EMBL; X57796; CAA40936.1; -;  
 DR EMBL; L26349; AAA59361.1; -;  
 DR EMBL; M76656; AAA40465.1; -;  
 DR EMBL; M88067; AAA40465.1; JOINED.  
 DR EMBL; M76655; AAA40465.1; JOINED.  
 DR EMBL; BC004592; AAA04591.1; -;  
 DR PIR; A38634; GQMSTL.  
 DR PIR; S16677; S16677.  
 DR PIR; S19021; S19021.  
 DR HSSP; P19438; 1EXT.  
 DR MGSP; MG1:131484; Tnfalfa.  
 DR InterPro; IPR000468; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR Pfam; PF00531; death; 1.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 454  
 FT  
 FT DOMAIN 22 212  
 FT TRANSMEM 213 235  
 FT DOMAIN 236 454  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 339 349  
 FT DOMAIN 356 441  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 195  
 FT DISULFID 185 191  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 202 202  
 FT CONFLICT 394 394  
 SQ SEQUENCE 454 AA; 50129 MM; 0710C2B8C32B6D9 CRC64;  
 Query Match 72.3%; Score 680; DB 1; Length 454;  
 Best Local Similarity 71.3%; Pred. No. 6.2e-50;  
 Matches 112; Conservative 19; Mismatches 26; Indels 0; Gaps 0;  
 Cy 1 DSVCPQGGKVIHPQNNNSICCKKCKGKGYLVNDGPGPODITDCEGSGSTASENLRHCL 60  
 Db 41 DSLCPQGGKVIHASKNSICCTCKCKKGYLVSDCPSPRDTVCCECEKGYTVAQNTLRVCL 100  
 Cy 61 SCSKCRKEMQVEIISCTVDRTVCGCRKQYRHYVSENLPOCFNCSCLNTVHLSCE 120  
 Db 101 SCKTRKEMSGVEISPPQADKDTVCGCKENQFORVLSHFQCVDPSPFNTVTLIPCKE 160  
 Cy 121 KQNTVCTCHAGFLRRENECVSGNSCKSLSECTYCLIP 157  
 Db 161 TQNTVCHAGFLRRESECVPSCHCKRNECMKCLIP 197  
 RESULT 4  
 TRIA BOVIN STANDARD; PRT; 471 AA.  
 ID TRIA BOVIN  
 AC 019131;







[illegible]

Query Match	Query Local Similarity	21.3%	Score 200.5	DB 1	Length 4117
Matches 46	Conservative 20	Mismatches 72	Indels 21	Gaps	
De	11	HPGNNSITCTKTHKTYIYNDPDPGPDNDPCPECSGSPFASENHP- HCLISGSKPKEM 69			TRHGWPKPLVTADACGMEALTEPPATHTSPDLSAHTLL PPDSKIKCTYOLV -> PPSIAGAPGAVQSVPLSVAG GVGVAVLWRVLELMTGSKVRKVKCATGTGHPAPASVULGR APGMPGPPRPMGHPDHLIPPLLSAQATGYCR (IN ISOFORM 12)
Oy	70	GVVSISSCTVDRLVCCCRNGYRHWSENLYC-----FNSLCLN-GTYH---LSQ 119			MISSING (IN ISOFORM 12) MEMVAVLLAGLVPLPILCATITLYTRHGWPKPLVTADACG MEALTEPPATHTLS -> SKMVCANAPFPTMLEDEAC
Db	100	SQVLENCMSAVADRCCKCKKFWEC---QVSQVSSSPFYCPCLDCAALRHRTLLCS 156			
Oy	120	EKQNTVCTCHAGFPLRENEVSC-----SNCKSLCTCYLC 155			
De	157	RNDTDCITCLGFEYHODGVCSPTSLSCPE--RCAVVC 195			
RESULT 8					
TR22_MOUSE	STANDARD	PRT	180 AA.		
1D	TR22_MOUSE	STANDARD	PRT	180 AA.	
AV	HEPCT_09CCT4_08VH9				
DM	15-JUN-2002 (Rel. 41, Created)				
DC	15-JUN-2002 (Rel. 41, Last sequence update)				
TC	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor receptor subfamily member 22 (Tumor necrosis factor receptor p60 homolog 2) (TNF receptor family member SOBA).				
GN	TNFRSF22 OR TNFRSF10 OR TNFRH2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
R2	SEQUENCE FROM N.A.				
RC	STRAIN=129/SV; TISSUE=Embryonic stem cells;				
FZ	MEHLIN=335/329, PubMed 10561328.				
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,				
LA	Laepe N., Reik W., Walter J.;				
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region;				
RT	implications for a novel imprinting centre and extended imprinting.";				
PL	Hum. Mol. Genet. 9:2691-2706(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Risser P., Mao W., Baldwin D.T., Pan G.;				
RT	"Characterization of SOBA, a murine member of the TNF family.";				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
FP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Embryo;				
FZ	MEDLINE=1085660; PubMed 11217851.				
RA	Kawai J., Shingawa A., Shibata Y., Yoshino M., Itoh M., Ishii Y.,				
RA	Aizawa T., Hara M., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,				
RA	Atawa K., Izawa M., Nishi K., Kiyosawa H., Tomo S., Yamanaka I.,				
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kaubukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,				
RA	Kochi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schiraldi L., Stadhli F., Suzuki R., Taita M., Wajner L., Washi T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Roffilli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ping B., Pingwah M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato Y., Schencksch C., Seya T., Shibata Y., Storch K.-F.,				

RA Suzuki H., Toyooka K., Wang K H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RL "Functional annotation of a full-length mouse cDNA collection.";   
 RL Nature 409:685-690(2001).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
 CC  
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 CC  
 DR EMBL; AJ278265; CAC16406.1; -  
 DR EMBL; AJ276505; CAC27353.1; -  
 DR EMBL; AY046551; AAL05073.1; -  
 DR EMBL; AK012838; BAB28502.1; -  
 DR HSSP; P19438; 1EXT.  
 DR MGD; MGI:1930270; Tofrsf22.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR SMART; SM00298; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2.  
 KW Receptor; Signal anchor; Transmembrane; Glycoprotein; Repeat  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL). Repeat  
 FT TRANSMEM 21 41 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 42 180 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 47 82 TNFR-CYS 1.  
 FT REPEAT 84 124 TNFR-CYS 2.  
 FT REPEAT 125 165 TNFR-CYS 3.  
 FT DISULFID 48 59 BY SIMILARITY.  
 FT DISULFID 60 73 BY SIMILARITY.  
 FT DISULFID 63 82 BY SIMILARITY.  
 FT DISULFID 85 100 BY SIMILARITY.  
 FT DISULFID 103 116 BY SIMILARITY.  
 FT DISULFID 106 124 BY SIMILARITY.  
 FT DISULFID 126 141 BY SIMILARITY.  
 FT DISULFID 144 157 BY SIMILARITY.  
 FT DISULFID 147 165 BY SIMILARITY.  
 FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 158 158 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 12 12 L -> V (IN REF. 3).  
 FT CONFLICT 171 180 RRSASVAVPI -> NERNRLFLLL (IN REF. 2).  
 SQ SEQUENCE 180 AA; 20226 MW; 45656:65A05AFA CRC64;  
 Query Match 21.1%; Score 198.5; DB 1; Length 180;  
 Best Local Similarity 32.8%; Pred. No. 3.6e-10;  
 Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;  
 QY 4 CPGKVIHPDNNSICTVCHVSTVLYNDGPGQDTCPECSSTFASENHLPHCLSCS 63  
 DB 48 CPAGEY...WSKDVCKKCSACFTVWAPCE:PHTQGGQEKYCHFTFTKFNLDACILCS 104  
 QY 64 KPFVFWGVFISCCVDRPTVCGGPFNVPVHYWSENLPQCNCGLCLNG TVILSCQEKQ 122  
 DB 105 TQEDP--GEMVADSATSPPGCPCTGLY-YDPPFPESCPCTYCPGGIFVLQCNSTA 161  
 QY 123 NTVCT 127  
 DB 162 NTVCS 166  
 RESULT 9  
 TNFR\_HUMAN  
 ID TNFR\_HUMAN STANDARD; PRT; 435 AA.  
 AC P16941.  
 DT 01-JUN 1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 3 precursor;  
 DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related  
 DE protein) (Tumor necrosis factor C receptor).  
 GN LTBP OP TNFSPF3 OP TNFPCP  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RN TISSUE=Liver;  
 RN MEDLINE=93252381; PubMed=8486360;  
 RA Paens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.,  
 RA "Construction and evaluation of a hncDNA library of human L2P  
 RA transcribed sequences derived from a somatic cell hybrid";  
 RT Genomics 16:214-218(1993).  
 RL [2]  
 RL SEQUENCE FROM N.A.  
 RL TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN FUNCTION  
 PP MEDLINE=94252509; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,  
 RA "A lymphotoxin-beta-specific receptor";  
 RL Science 264:707-710(1994).  
 RN [4]  
 RN CHARACTERIZATION  
 PP MEDLINE=99231511; PubMed=10207006;  
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
 RA "The cytoplasmic domain of the lymphotoxin beta receptor mediates cell  
 RA death in HeLa cells";  
 RL J. Biol. Chem. 274:11868-11873(1999).  
 RN [5]  
 RN FUNCTION.  
 PP MEDLINE=20261554; PubMed=10799510;  
 RA Poorey I.A., Butrovich K.D., Glass A.A., Ertugroglu S., Benedict C.A.,  
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;  
 RA "The lymphotoxin-beta receptor is necessary and sufficient for  
 RA LIGHT-mediated apoptosis of tumor cells";  
 RL J. Biol. Chem. 275:14307-14315(2000).  
 CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
 CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
 CC and TRAF5. May play a role in the development of lymphoid organs  
 CC and TRAF5. Self-associates.  
 CC -!- SUBUNIT: Self-associates.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: CONTAINS 4 TNFR CYS REPEATS.  
 CC  
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 CC  
 DR EMBL; L04270; AAA36757.1; -  
 DR EMBL; BC026562; AAA26562.1; -  
 DR HSSP; P25942; 1CDF.  
 DR Genew; HGNC:6718; LTBR.  
 DR MIM; 600979; -  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 4.  
 DR ProDom; PD000771; TNFR\_C6; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; SIGNAL  
 FT SIGNAL 1 30 POTENTIAL.





Dh 141 KONTVCRCPCGCTYSDEANHVDPCLPCTVCEDTERQLRECTR 182

## RESULT 11

```

TR16 MOUSE STANDARD: PPT; 417 AA.
AC Q920W1;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
DE affinity nerve growth factor receptor) (NGF receptor) (low affinity
DE neurotrophin receptor p75NTR)
GN NGFR OR TNFRSF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N A
RC STRAIN=A;
RX MEDLINE=99077793; PubMed=9857182;
RA Tuffreau C, Renejean J, Blondel D, Kieffer B, Flament A;
RT "Low affinity nerve growth factor receptor (p75NTR) can serve as a
RT receptor for rabies virus.";
RL EMBO J. 17:7250-7259(1998).
CC -!- FUNCTION: low affinity receptor which can bind to NGF, BDNF, NT 3,
CC AND NT-4. Can mediate cell survival as well as cell death of
CC neural cells (By similarity). Binds to rabies virus glycoprotein
CC Gs.
CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- PTM: N- AND O-glycosylated (By similarity).
CC -!- PTM: Phosphorylated on serine residues (By similarity).
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
DR EMBL; AF105292; AAD17943 1; -
DR RSP; P07174; INGP
DR MGP; MGI:97323; Ngfr.
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; death; 1
DR Pfam; PF00200; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 417 TNFRP NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 16.
FT DOMAIN 22 246 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 247 265 POTENTIAL.
FT DOMAIN 266 417 CYTOPLASMIC (POTENTIAL).
FT REPEAT 24 57 TNFR-CYS 1.
FT REPEAT 59 100 TNFR-CYS 2.
FT REPEAT 101 139 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 346 411 DEATH.
FT DOMAIN 190 241 SER/THR-PTCH
FT DISULFID 25 36 BY SIMILARITY

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FT DISULFID 37 50 BY SIMILARITY.
FT DISULFID 40 57 BY SIMILARITY.
FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 79 92 BY SIMILARITY.
FT DISULFID 82 100 BY SIMILARITY.
FT DISULFID 102 115 BY SIMILARITY.
FT DISULFID 118 131 BY SIMILARITY.
FT DISULFID 121 139 BY SIMILARITY.
FT DISULFID 142 157 BY SIMILARITY.
FT DISULFID 160 173 BY SIMILARITY.
FT DISULFID 163 181 BY SIMILARITY.
FT CAPBOHYD 53 53 N-LINKED (GLUCNA... (POTENTIAL).
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DB9AFB2 CRC64;

Query Match 19.1%; Score 181.5; DR 1; Length 417;
Best Local Similarity 31.5%; Pred. No. 1.9e-08;
Matches 51, Conservative 25, Mismatches 67, Indels 19; Gaps 10;

Qy 4 CPOGKYIHPONNISCTCKHGTLYNDTPGPGTCTCTREC-ESGFTASENHLRHLSG 62
| | | | | | | | | | | | | | | | | | | | | |
Db 25 CSTGMVTH--SGECYACNLGRTVAQC-GANG TVCEPCLDSVTFSDVAVATENKRY 79
| | | | | | | | | | | | | | | | | | | | | |

Qy 53 SKCPKEMQVEISS-CTVDPDTVCTGTPENYEHYKSENLPQCFNSGLCLNLT VHSGLQF 120
| | | | | | | | | | | | | | | | | | | | | |
Db 90 TEC---LGLQSMRAPVVEADDAVTPC---SYVYVQDEFTTETREANLVCTVGSGLVENVQD 133
| | | | | | | | | | | | | | | | | | | | | |

Qy 121 KONTVC TCHAGFELPE -NECVSCSNVYFSEVCTFLCLP 157
| | | | | | | | | | | | | | | | | | | | | |
Db 134 KONTVCCEEGTGYSDANHVDPCLPCTVCEDTERQLRECTP 175
| | | | | | | | | | | | | | | | | | | | | |

RESULT 12
TR1B MOUSE STANDARD: PPT; 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae, Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.;
RA Wong G.H., Chen E.Y., Goeddel D.V.;
PT "Cloning and expression of cDNAs for two distinct murine tumor
PT necrosis factor receptors demonstrate one receptor is species
PT specific.";
RL Proc. Natl. Acad. Sci. U S A 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE OF 1-26 FROM N.A.
RX STRAIN=NOD;
RA Jacob C.O., Liu J.;
PL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RX TISSUE=Liver;
RA Kissinger M., Fellows R., Feldmann M., Chernaiovsky Y.;
PL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor with high affinity for TNFR2/TNF alpha and

```



Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7.

QY 13 QNNSICCTCKHKTLYNDQPCGGQDQPCPCESGSPPTASENLPHGLSC-SKCPKEMGO 71  
 DB 34 EKDGCTCTCPGASVSLC-GPGSDTVCSCKNETFTASTNHAPACVCRGCTGHLS- 91  
 QY 72 VEISSCTVDRPTVCGKNOYRHHWYSHNLCCFNCISCLNTVHLSQCFKNTVCTHAG 141  
 DB 92 ESQCPDTHPVCNCSTGNVLLFGJN- ---GFCAPQT --- KATA 142  
 QY 132 PFLPENCVCSCNCF- ---ELECTRIC 155  
 DB 133 YGVSGHTRAGDTLCEKCPHTYSDLSPTERC 164

RESULT 15  
 TNR6\_PIG ID TNR6\_PIG STANDARD; PRT; 332 AA.  
 AC 07736;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
 GN TNFSP6 OP APT1 OP FAS  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suidae.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Batling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Baumer D., "Expression of apoptosis-associated genes in hibernating and stunned myocardium of pig";  
 RT Submitted (JAN-1998) to the EMBL/GenBank/DDRJ databases.  
 PL FUNCTION: Receptor for TNFSP6/FASL. The adaptor molecule FASD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase 8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FASD, AND MAYBE TO OTHER CYTOSOLIC APTAOR PROTEINS.  
 CC -!- SIMILARITY: CONTAINS 3 TNF-CYS REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7.

QY 13 QNNSICCTCKHKTLYNDQPCGGQDQPCPCESGSPPTASENLPHGLSC-SKCPKEMGO 71  
 DB 34 EKDGCTCTCPGASVSLC-GPGSDTVCSCKNETFTASTNHAPACVCRGCTGHLS- 91  
 QY 72 VEISSCTVDRPTVCGKNOYRHHWYSHNLCCFNCISCLNTVHLSQCFKNTVCTHAG 141  
 DB 92 ESQCPDTHPVCNCSTGNVLLFGJN- ---GFCAPQT --- KATA 142  
 QY 132 PFLPENCVCSCNCF- ---ELECTRIC 155  
 DB 133 YGVSGHTRAGDTLCEKCPHTYSDLSPTERC 164

RESULT 14  
 VT2 SFVKA ID VT2 SFVKA STANDARD; PRT; 325 AA.  
 AC P25943;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor soluble receptor precursor (Protein T2)  
 GN T2.  
 OS Shope fibroma virus (strain Kasza) (SFV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Leporipoxvirus  
 OX NCBI\_TaxID=10272;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87321103; PubMed=2820128;  
 RA Upton C., Delange A.M., McPadden G.;  
 RT "Tumor necrosis factor soluble receptor precursor";  
 RT Telomeric region of the Shope fibroma virus genome";  
 RL Virology 160:20-30(1987).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=91207415; PubMed=1850261;  
 RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,  
 RA McPadden G., Goodwin P.G.;  
 RT "T2 open reading frame from the Shope fibroma virus encodes a soluble form of the TNF receptor";  
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991)  
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.  
 CC -!- SIMILARITY: CONTAINS 4 TNF-CYS REPEATS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -!- NOT ANNOTATED\_CDS.  
 DR EMBL; A21727; CAA01687.1; -  
 DR PIR; R43692; R43692.  
 DR HSSP; P19438; 1EXT.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6\_2  
 DR ProDom; PD000771; TNFR\_c6\_1.  
 DR SMART; SM00208; TNFR\_1  
 DR PROSITE; PS006452; TNFR\_NGFR\_1, 2  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 1  
 KW Receptor; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR

FT REPEAT 27 62 TNFR-CYS 1.  
 FT REPEAT 63 104 TNFR-CYS 2.  
 FT REPEAT 105 147 TNFR-CYS 3.  
 FT REPEAT 148 186 TNFR-CYS 4.  
 FT DISULFID 28 39 BY SIMILARITY.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 43 61 BY SIMILARITY.  
 FT DISULFID 64 79 BY SIMILARITY.  
 FT DISULFID 82 96 BY SIMILARITY.  
 FT DISULFID 86 104 BY SIMILARITY.  
 FT DISULFID 106 120 BY SIMILARITY.  
 FT DISULFID 123 146 BY SIMILARITY.  
 FT DISULFID 129 149 BY SIMILARITY.  
 FT DISULFID 164 185 BY SIMILARITY.  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 325 AA; 35132 MW; 81030339198A71E CRC64;

Query Match 18.9%, Score 178, DB 1; Length 326;  
 Best Local Similarity 29.6%, Prev No. 30-08;  
 Matches 45; Conservative 15; Mismatches 62; Indels 40; Gaps 6;  
 QY 13 QNNSICCTCKHKTLYNDQPCGGQDQPCPCESGSPPTASENLPHGLSC-SKCPKEMGO 71  
 DB 34 EKDGCTCTCPGASVSLC-GPGSDTVCSCKNETFTASTNHAPACVCRGCTGHLS- 91  
 QY 72 VEISSCTVDRPTVCGKNOYRHHWYSHNLCCFNCISCLNTVHLSQCFKNTVCTHAG 141  
 DB 92 ESQCPDTHPVCNCSTGNVLLFGJN- ---GFCAPQT --- KATA 142  
 QY 132 PFLPENCVCSCNCF- ---ELECTRIC 155  
 DB 133 YGVSGHTRAGDTLCEKCPHTYSDLSPTERC 164

RESULT 15  
 TNR6\_PIG ID TNR6\_PIG STANDARD; PRT; 332 AA.  
 AC 07736;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
 GN TNFSP6 OP APT1 OP FAS  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suidae.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Batling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Baumer D., "Expression of apoptosis-associated genes in hibernating and stunned myocardium of pig";  
 RT Submitted (JAN-1998) to the EMBL/GenBank/DDRJ databases.  
 PL FUNCTION: Receptor for TNFSP6/FASL. The adaptor molecule FASD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase 8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FASD, AND MAYBE TO OTHER CYTOSOLIC APTAOR PROTEINS.  
 CC -!- SIMILARITY: CONTAINS 3 TNF-CYS REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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CM protein protein search, using sw model

Run on: January 6, 2003, 03:47:44 ; Search time 28 Seconds  
(without alignments)  
1184 771 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 PSVCPQKQYHPQNNISICT.....GNSCKYFSLCTKLCPLQIEN 161

Scoring table: BL0SUM62

Gapop 10 0 , Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

DB base :

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phase:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rivirus:
- 16: sp\_bacteriaph:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	780	82.9	446	6	Q95ND3	Q95nd3 felis silve
2	756	80.3	189	6	Q97530	Q97530 canis famil
3	731	77.7	189	6	Q95185	Q95185 felis silve
4	202	21.5	413	11	Q93MM1	Q93mm1 mus musculu
5	193	20.5	387	13	Q97VD4	Q97vd4 xenopus lae
6	191	20.3	413	11	Q912M6	Q912m6 rattus norv
7	188	20.0	302	13	Q9PUS0	Q9pus0 salvelinus
8	182.5	19.4	285	13	Q9DGH7	Q9dgh7 gallus gall
9	179.5	19.1	357	13	Q9EF34	Q9ef34 brachydanio
10	176.5	18.8	320	12	Q57079	Q57079 cowpox viru
11	176	18.7	459	11	Q62327	Q62327 mus musculu
12	175.5	18.7	312	13	Q9DGH8	Q9dgh8 gallus gall
13	175.5	18.7	322	12	Q72761	Q72761 cowpox viru
14	171.5	18.2	316	12	Q57092	Q57092 ectromelia
15	171.5	18.2	320	12	Q57091	Q57091 ectromelia
16	171.5	18.2	320	12	Q57300	Q57300 ectromelia

ALIGNMENTS

RESULT 1

Q95ND3 ID Q95ND3 PRELIMINARY; PRT: 446 AA.

AC Q95ND3; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Tumor necrosis factor type I.  
GN TNFR I.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
PA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsurimoto H.;  
RT "Molecular cloning of feline tumor necrosis factor receptor type I  
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in  
RT cats";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051103; BAB55455.1; ...  
DR InterPro; IPR000345; Cyt\_heme\_bind.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death\_1...  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00181; EGF\_1.  
DR PROSITE; PS00190; CYTOCHROME C, UNPROW...  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
DR PROSITE; PS09652; TNFR\_NGFP\_1; UNPROW...  
DR PROSITE; PS00050; TNFR\_NGFP\_2; 3.  
SQ SEQUENCE 446 AA, 49563 MW, 2178D331DD8A74AA CRC64;

Query Match 82.9%; Score 780; DR 6; Length 446;  
Best Local Similarity 84.1%; Pct. No. 1,5e-78;  
Matches 135; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

[illegible]

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CX	NCBI_TaxID=9685;
RN	(1)
RP	SEQUENCE FROM N.A.
RA	Duthe S., Nasir L., Eckersall P.D.;
RT	"Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RT	partial cds.";
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U72344; AAB5089.1; -.
DR	HSSP; P19438; TEXT.
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 3.
DR	SMART; SM00208; TNFR_3.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DK	PROSITE; PSS0050; TNFR_NGFR_2; 3.
KW	Receptor.
FT	NON TER
SO	SEQUENCE 189 AA; 189
	Query Match 77.7%; Score 731; DB 6; Length 189;
	Best Local Similarity 85.5%; Pred. No. 1.8e-73;
	Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
OY	4 CPQKYLHPNNNSICCTCKHKGTYLYNCPGQDTPDCRECSGSFASNNHLRHLCSS 63
DB	44 CPQKYLHPNDNSICTCKHKGTYLYNCEPGLDTPCREENGTFFASNNYLRQLSSS 103
OY	64 KCRKMGQVEISSCTVDKDTVCGRKKNQRYHWSBNLPQCPNCSLCINGTVHLSGCKEK 123
DB	104 KCRKEMQVEISPTGYRDTVCGRKKNQRYHWSNTHPQCLNCSLCINGTVQISCEYET 163
OY	124 TVCTCHAGFPLRENECVSCSNCKS 148
DB	164 TVCTCHAGFPLRGNECVSCNCKKN 188
RESULT 4	
O39MM1	IFELIMINAFY; FRT; 413 AA.
1J	O39MM1
AC	O39MM1;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	WSP-1-like protein.
GN	TNFRSF12.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STEPAINE=129/SV;
RX	MEDLINE=21158384; PubMed=11261933;
RA	Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RT	Owen M.D.;
RT	"genomic structure, expression, and chromosome mapping of the mouse
RT	gene.";
RL	Immunogenetics 53:59-63(2001).
ER	EMBL; AF329669; AAK11256.1; -.
ER	HSSP; P25942; 1CDF.
ER	MGD; MGI:193467; Tnftrsf12.
ER	InterPro; IPR000488; Death.
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00031; death_1.
DR	Pfam; PF00030; TNFR_c6; 3.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00208; TNFR_3.
DR	PROSITE; PSS0017; DEATH DOMAIN; 1.

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DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABAF CRC64,

Query Match 21.5%; Score 202; DB 11; Length 413;
Best Local Similarity 31.4%; Pred No 2 3e-14;
Matches 48; Conservative 19; Mismatches 58, Indels 28, Gaps 7,

QY 18 CCTKTKTKTYLYNCPGPGQDTCPGPGSGSFTASENHLR-HGLSCSKCPKEMGVGEISS 76
DB 54 CUREGPGHYKAPCAEDCGNSTLPTSTLTLPNNHFTDTPCQVTEALQVTLN 113
QY 77 CTVDRTVCGCKQKQRYHWSENFQCFNCSLCLNG-TVHLSC-----QFKQNTVCT 127
DB 114 CSAKSDTHCGGQSG-----W-----CVD-STVPCGKSSPFCVPGATTPTVHEAPTRP 162
QY 128 CHAGFFLENECVSC-----SNCKKSLECTKLC 155
DB 163 CLPGEVYRGNDCTSCPTGFSVCPKA--CTAVC 193

RESULT 5
Q9PVD4 PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01 MAY-2000 (Tremblrel. 13, Created)
DT 01 MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01 JUN-2001 (Tremblrel. 17, Last annotation update)
DE P75 like transmembrane protein fullback.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
OC Amphibia; Batrachia, Anura, Mesobatrachia, Pipidea, Pipidae,
OC Xenocephalidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hick P., Sun R.T., Collins-Paie L., LaVallie E., Sive H.L.;
RT "Identification and Characterization of fullback, a Novel Posteriorly-
RT Expressed Xenopus Gene".
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131850; AAC54072 1,
DR HSSP; P07174; INGR.
DR InterPro; IPR001081; Copper-fist
DR InterPro; IPR000488; Death
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00412; C1_FIST; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 20.5%; Score 193; DB 13; Length 387;
Best Local Similarity 31.9%; Pred No 2 2e-13;
Matches 53; Conservative 24; Mismatches 71, Indels 18, Gaps 10,

QY 1 DSVCPQRYVHPQNNISICTYCHKTYLYNCPGPGQDTCPGPGSGSFTASENHLPHC 59
DB 22 EAVVEEGLY---TNGKGCSCGAPAGVWVPC--GDSNTCFRCIENSTFSDVPSAPAK 76
QY 60 LSCSKCPKEMGVGEISSCTVDRTVCGCKQKQRYHWSENFQCFNCSLCLNG-TVHLSC 118
DB 77 CUREGPGHYKAPCAEDCGNSTLPTSTLTLPNNHFTDTPCQVTEALQVTLN 131
QY 119 QFKQNTVCTCHAGFFLENECVSC-----ENECVSC-SNCKKSLECTKLC 158
DB 132 THNKNTVCLQSSGYSYSEVWSSFSPTCPTEQVTEVQIGDGVCP 177

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RESULT 6
Q912M6 PRELIMINARY; PRT; 433 AA.
AC Q912M6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01 MAR-2002 (Tremblrel. 20, Last annotation update)
DE Tumor necrosis factor receptor type II (Fragment).
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Buckel H.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF alpha transport
RT through the blood-brain barrier."
PL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021 1,
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR Receptor.
DR NON_TER 1 1
DR NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 20.3%; Score 191; DB 11; Length 433;
Best Local Similarity 32.7%; Pred. No. 4e-13;
Matches 52; Conservative 18; Mismatches 79, Indels 16, Gaps 7,

QY 4 CPQGYVHPQNNISICTYCHKTYLYNCPGPGQDTCPGPGSGSFTASENHLPHC 62
DB 20 CQISQEVYVYACMGAPCPGPGVAFHPCNPTSDVWALCAAGMFQVNNHHTLNS 74
QY 63 SKCFKEMGVGEISSCTVDRTVCGCKQKQRYHWSENFQCFNCSLCLNG-TVHLSC 119
DB 79 SSCSDG--QVETHCTFKQNFVTAHAGSYALFELKGR-FJWELKGR-HHAFAP 136
QY 120 EYQNTVCT-CHAGFFLENECVSCSNCFYSLEETKLC 157
DB 137 SNGNVICSACAPSTF--SDTTSSTDVCRPHRIGSILAIP 173

RESULT 7
Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01 JUN-2002 (Tremblrel. 21, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Tricacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation."
RL Biol. Reprod. 42:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSP; O14763; ID4V.
DR InterPro; IPR000561; EGF like.
DR InterPro; IPR001368; TNFR_C6.

```





RA Pickup D.J., Bastia D., Stone H O., Joklik W K ;  
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of  
 RT repeated and unique sequence elements."  
 RL Proc Natl Acad Sci U S A 73:7112-7116(1982).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=90177240; PubMed=2109453;  
 RA Parsons B.L., Pickup D.J.;  
 RT "Transcription of orthopoxvirus telomeres at late times during  
 RT infection.";  
 RL Virology 175:69-80(1990).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=91196263; PubMed=2014645;  
 RA Hu F.Q., Pickup D.J.;  
 RT "Transcription of the terminal loop region of vaccinia virus DNA is  
 RT initiated from the telomere sequences directing DNA resolution.";  
 RL Virology 181:716-720(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RX MEDLINE=94378510; PubMed=8091665;  
 RA Hu F.Q., Smith C.A., Pickup D.J.;  
 RT "Cowpox virus contains two copies of an early gene encoding a soluble  
 RT secreted form of the type II TNF receptor";  
 RL Virology 204:343-356(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RA Pickup D.J.;  
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRIGHTON RED;  
 RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U87234; AAB94344.1 ;  
 DR EMBL; AF482758; AAM13659.1 ;  
 DR HSSP; 014763; 1DOG.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SMO0208; TNFR; 2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor.  
 SQ SEQUENCE 320 AA; 35234 MW; AADDFCPC47F7A86 CRC64;

Query Match 18.8%; Score 176.5; DB 12; Length 320;  
 Best Local Similarity 27.8%; Pred. No. 1.2e-11;  
 Matches 42; Conservative 22; Mismatches 62; Indels 25; Gaps 6,  
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 Db 38 SNNLCCKQCDPGMYMTHSCNTTSNKKCKDPDFTTSIPNHPCTCSCGKCK--SSNHV 94  
 QY 73 ELSCTVDPTGCGCFKFNYPHYWSENIPQCFNCLNGTGVHLSCQFQNTVCTCHAGF 132  
 Db 95 ETKSCSNTQDVGVASGYCFRFGSN-----GPFICVPGT-----KCDGGY 136  
 QY 133 FL---PENEVCSCNCKKSLFTKLCLEQIE 160  
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 DT 01 NOV 1996 (TREMBLrel. 01, Created)  
 DT 01 NOV 1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN 2002 (TREMBLrel. 21, Last annotation update)

DE Murine tumour necrosis factor receptor 2 protein (Fragment).  
 GN TNFRSF1B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD;  
 RA Powell E.B., Wicker L.S., Peterson L.B., Todd J.A.;  
 RT "Amino acid variation in the tumor necrosis factor receptor 2 is  
 RT linked to autoimmune diabetes in NOD mice.";  
 RL Genomics 0:0-0(0).  
 RN [2]  
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 RC STRAIN=NOD;  
 RX MEDLINE=95178848; PubMed=7873884;  
 RA Powell E.B., Wicker L.S., Peterson L.B., Todd J.A.;  
 RT "Allelic variation of the type 2 tumor necrosis factor receptor  
 RT gene.";  
 RL Mamm. Genome 5:726-727(1994).  
 DR EMBL; X76401; CAA53981.1 ;  
 DR HSSP; P19438; INCF.  
 DR MGD; MGI:1314883; Infrsfib.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
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 FT NON\_TER 1 1  
 FT VARIANT 87 87 S -> T.  
 FT VARIANT 93 93 T -> I.  
 FT VARIANT 268 268 F -> I.  
 FT VARIANT 345 345 S -> F.  
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 QY 63 SKCRKEMGQVELSCTVHPPTVCGPENVY----PHYWSENLPFCNCLNGTGVHL 119  
 Db 84 SSCSTD--QVETRACTQQQNVCAEAGPYCALKTH SSCCFQCPPLSKGGHGVANS 139  
 QY 118 COEKONTVC--CHAGFFLFEHCVCSCCKKSGLECTVLCIF 167  
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RESULT 12  
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 ID Q9DGH8 PPELIMINARY; PRT; 312 AA.  
 AC Q9DGH8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 18, Last annotation update)  
 DE Fas antigen (Fragment).  
 GN FAS.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bridgman J.T., Johnson A.L.;  
 RT "Fas Expression and Regulation in Hen Granulosa Cells.";







GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 04:09:12 ; Search time 2808 Seconds  
(without alignments)  
1668.644 Million cell updates/sec

Title: US-09-882-735-2  
Perfect score: 941  
Sequence: 1 DSVCPQKYYHPQNNISICT CSNCKKSEETKICLPQIEN 161

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database :

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9: gb\_pr :  
10: gb\_ro :  
11: gb\_sts :  
12: gb\_sy :  
13: gb\_un :  
14: gb\_vl :  
15: em\_ba :  
16: em\_fun :  
17: em\_hum :  
18: em\_in :  
19: em\_mu :  
20: em\_ov :  
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23: em\_pat :  
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28: em\_un :

29: em\_vl :  
30: em\_htg\_hum :  
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32: em\_htg\_other :  
33: em\_htg\_mus :  
34: em\_htg\_pln :  
35: em\_htg\_rod :  
36: em\_htg\_mam :  
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38: em\_sv :  
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41: em\_htgo\_other :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	941	100.0	483	6	AR174442 Sequence
3	941	100.0	1301	6	AR1131310 Sequence
4	941	100.0	1301	6	AR1131310 Sequence
5	941	100.0	1331	6	A29103 H. sapiens m
6	941	100.0	1368	6	A29098 Sequence 1
7	941	100.0	2050	9	M60375 Human tumor
8	941	100.0	2062	6	A21522 TRF alpha 1
9	941	100.0	2062	6	143805 Sequence 24
10	941	100.0	2087	9	HUMTNFR
11	941	100.0	2109	9	AF956611 M31294 Human tumor
12	941	100.0	2111	6	A26412 cDNA for
13	941	100.0	2111	6	AX409713 Sequence
14	941	100.0	2111	9	HUMTNFRB
15	941	100.0	2112	9	HUMTNFRB
16	941	100.0	2161	6	AP006330 M61121 Human tumor
17	941	100.0	2161	9	HSTNFR1A X55113 H. sapiens
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19	941	100.0	2175	6	A78738 Sequence 7
20	941	100.0	2175	6	AR041076 Sequence 1
21	941	100.0	2175	6	164751 Sequence 1
22	941	100.0	2176	6	A19207 AR010140 Homo sapi
23	941	100.0	2194	9	BC010140 Sequence 2
24	941	100.0	6889	6	126928 AR041375 Sequence
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ALIGNMENTS

[illegible]

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 483)
TITLE	Bendele, A.M., Sennello, R.M. and Edwards III, C.K.
JOURNAL	Combination therapy using a TNF binding protein for treating
FEATURES	TNF-mediated diseases
SOURCE	Patent: US 6306830-A 1 23-0CC: 2001;
ORIGIN	Location/Qualifiers
BASE COUNT	130 a 124 c 123 g 106 t
ORIGIN	/organism="unknown"
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Score:	941.00
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Best Local Similarity:	100.00%
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Dp	181 AGCTGCTCCAAATGCGGAAAGGAGTGTGAGGTGATCTTCTTCCACAGTGGAC 240
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Dp	241 CCGGACACCGCTGTGTGTGCTGCAGGAAGAACCGATACCGGCACTTATTTGGATGAAAACCTT 300
QY	101 PheGlnCysPheAsnCysSerIeucysLeuGlnGlyThrValHisLeuSerCysGlnGlu 120
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DEFINITION	Sequence 7 from patent US 6193972.
ACCESSION	AR131310
VERSION	AR131310.1 GI:14120213
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1301)
	Campbell, R.K., Jameson, B.A. and Chappell, S.C.

TITLE Hybrid heterodimeric protein hormone  
JOURNAL Patent: US 6193972-A 7 27-FEB-2001;  
FEATURES Location/Qualifiers  
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BASE COUNT 269 a 413 c 351 g 268 t  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US 09-882 735-2 (1-161) x AR131310 (1-1301)

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QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
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Db 585 CGGAAATATGTAT 644  
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DEFINITION Sequence 7 from patent US 6194177.  
ACCESSION AR134762  
VERSION AR134762.1 GI:14123667  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1301)  
TITLE Campbell, R. K., Jameson, R. A., and Chappel, S. C.  
JOURNAL DNA encoding a hybrid heterodimeric protein  
FEATURES Patent: US 6194177-A 7 27-FEB-2001,  
source Location/Qualifiers  
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US 09-882 735-2 (1-161) x AP134762 (1-1301)

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QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
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QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
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RESULT 5  
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LOCUS  
DEFINITION H.sapiens mRNA for TNF-binding polypeptide from patient EP0494448  
ACCESSION A29103  
VERSION A29103.1 GI:1247517  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1331)  
AUTHORS Hauptmann, R., Himmler, A., Maurer-Pegib, I., and Striatowa, J.  
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
JOURNAL Patent: EP 0394348-A 3 24-OCT-1990;  
FEATURES BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H.  
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significantly

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275. .1513

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Best local Similarity:	100.00%	Mismatches:
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US 09 882-735-2 (1-161) x HUMTNERP (1-2050)

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DB 195 TGGAGGAGTGTGATAGAGGAGGAGTCTTTAAATGTTCAAGAAAGCAGCTTTAGAGAGCTGCTT 454

607

Q. Now, you're going to tell me that the defendant was not in the car at the time of the shooting, is that correct?

455 AAGTGGTCGAAATGCTGAAAGTAAATGCTGACATCTTTCTTGACAGTGGAC 514

Qy H1 ArgAspThrValCysGlyCysArgGlyAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100

[illegible]

101 Photocopying by any means without the written permission of the publisher is prohibited.

[illegible]

639

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635 AAACAGAA

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ORIGIN

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Mismat che	
Indels:	
Gaps:	

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Db	275	CATAGTGTGTCTCCCAAGCAAAACATATGAGGCAAGCAAAATAATTCATTTGGTGGTGA	344
QY	21	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	40
Db	335	AAGTGGCAACAAAGAACTATTTATCAATCACTGCAAGTGGAGCAAGCAACGAA	394
QY	41	CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	60
Db	395	TGCAAGAGAGTGTGAGAGTGGACTATTCAAGGTTTAAACAAACAAGCAAAATGAGCTC	454
QY	61	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp	80
Db	455	AGCTGTCTCCAAATGCTCAAGAGAAATGGTCAAGTCAATCTTTCTTCTGCAAGCAAA	514
QY	81	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu	100
Db	515	CGGACACACCGTGTGTGTGTATCAAGCAAAACAGTACAGCAATATGAGCAACAAAA	574
QY	101	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnIleu	120
Db	575	TTCAGAGTGTCTCAATTCAAGCTGTCTCAATGCAAGCTGTCAAGTCTCTCTCAAG	634
QY	121	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlyCysVal	140
Db	635	AAACAGACACCGGTGTGACCTCCATGACGTCTCTTCTAACAGAAAAACAGTCTCTC	694
QY	141	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleuLeu	160
Db	695	TCTGTGATTAATGTGAAGAAAAAGTTGAGTGAAGAGATTGTCACTATCACTCAATTG	754
QY	161	Asn 161	
Db	755	AAT 757	
RESULT 9			
443805			





Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-882-735-2 (1161) x AX49713 (1-2111)

QY 1 AspSerValCysProGlnGlyLeuTyrLeuHisProGlnAsnAsnSerIleCysCysThr 20  
DB 307 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCTCCAAATATATTCGATTGCTGTACC 366

QY 21 LysCysHisIysGlyTyrThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 367 AAGTCCCAAGAACGACCTACTGTATCAATGACTGTCACGGCCCGCCGACGATACGGAC 426

QY 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisIleuArgHisCysLeu 60  
DB 427 TGCAGGGAGTGTGAGAGGGCTCTTACCGCTTCACAAAACCACTCCAGACACTCCCTC 486

QY 61 SerCysSerIysCysArgGlySerGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
DB 487 AGTCTCTCAATATCCCGAAGGAAATGGTCAAGTGGAGATCTCTTCCGACAGTGGAC 546

QY 81 ArgAspThrValCysGlyCysArgGlyAsnGlnTyrArgHisIleTyrTrpSerGluAsnLeu 100  
DB 547 CGGACACCGGTGTGGTGTGAGGAAACAGACCGGATTAATATGAGTAAACCTT 606

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisIleuSerCysGlnGlu 120  
DB 607 TTCAGTCTCTCAATTTGAGGCTTGTCTCCATGGAGACCGTGCACCTCTTCCGACGAGG 666

QY 121 LysGlnAsnThrValCysThrCysHisIleGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 667 AACAGGAACCGGTGTGACCTGCAAGTGGTGGTCTTTTAAAGAAAGAAAGAGTGTGTC 726

QY 141 SerCysSerAsnCysIysIysSerLeuGluCysThrIleuSerCysLeuProGlnIleGlu 160  
DB 727 TCTGTACTACTGTAAAGAAAGCTGGAGTGCACCAAGTGTGCTTACCCAGATTGAG 786

QY 161 Asn 161  
DB 787 AAT 789

RESULT 14  
AX49713 2111 bp DNA linear PAT 14-JUN-2002  
LOCUS AX49713  
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION AX49713  
VERSION AX49713.1 GI:21442418  
KEYWORDS  
SOURCE Human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Alvarez, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.  
TITLE Gene expression profiles in liver cancer  
JOURNAL Parent: W0229133-A 2000 11:AFR-2002;  
GENE LOGIC INC (US)  
FEATURES  
source location/Qualifiers  
1..2111  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="EMBL/GenBank Accession No. M58286"

BASE COUNT 445 A 629 C 587 G 450 T  
ORIGIN  
Alignment Scores:  
Fred. No.: 2.46e 79 Length: 2111  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-882-735-2 (1161) x AX49713 (1-2111)

QY 1 AspSerValCysProGlnGlyLeuTyrLeuHisProGlnAsnAsnSerIleCysCysThr 20  
DB 307 GATAGTGTGTGTCCCAAGGAAAAATATATCCACCTCCAAATATATTCGATTGCTGTACC 366

QY 21 LysCysHisIysGlyTyrThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 367 AAGTCCCAAGAACGACCTACTGTATCAATGACTGTCACGGCCCGCCGACGATACGGAC 426

QY 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisIleuArgHisCysLeu 60  
DB 427 TGCAGGGAGTGTGAGAGGGCTCTTACCGCTTCACAAAACCACTCCAGACACTCCCTC 486

QY 61 SerCysSerIysCysArgGlySerGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
DB 487 AGTCTCTCAATATCCCGAAGGAAATGGTCAAGTGGAGATCTCTTCCGACAGTGGAC 546

QY 81 ArgAspThrValCysGlyCysArgGlyAsnGlnTyrArgHisIleTyrTrpSerGluAsnLeu 100  
DB 547 CGGACACCGGTGTGGTGTGAGGAAACAGACCGGATTAATATGAGTAAACCTT 606

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisIleuSerCysGlnGlu 120  
DB 607 TTCAGTCTCTCAATTTGAGGCTTGTCTCCATGGAGACCGTGCACCTCTTCCGACGAGG 666

QY 121 LysGlnAsnThrValCysThrCysHisIleGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 667 AACAGGAACCGGTGTGACCTGCAAGTGGTGGTCTTTTAAAGAAAGAAAGAGTGTGTC 726

QY 141 SerCysSerAsnCysIysIysSerLeuGluCysThrIleuSerCysLeuProGlnIleGlu 160  
DB 727 TCTGTACTACTGTAAAGAAAGCTGGAGTGCACCAAGTGTGCTTACCCAGATTGAG 786

QY 161 Asn 161  
DB 787 AAT 789

RESULT 14  
HUMTNFRB 2111 bp mRNA linear PRI 03-AUG-1993  
LOCUS HUMTNFRB  
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M58286 M33480  
VERSION M58286.1 GI:339753  
KEYWORDS tumor necrosis factor receptor  
SOURCE Human cell line Hu60, cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Leuchter, H., Par, Y. C., Loh, H. W., Gent, L. F., Brockhaus, M., Tabuchi, H. and Lesslauer, W.  
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor  
JOURNAL Cell 61 (2), 351-359 (1990)  
MEDLINE 90235284  
PUBMED 2158862  
FEATURES  
source location/Qualifiers  
1..2111  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/cell\_line="Hu60"  
1..2111  
/gene="TNF receptor"  
/gene="TNF receptor"  
187..1554  
/gene="TNF receptor"  
/note="55 kDa"  
/codon\_start=1  
/product="tumor necrosis factor receptor"  
/protein\_id="AA36753.1"  
/db\_xref="GI:339754"  
/translation="MGLSTVPDLPLPLVLELLVGIYPSVITGLVPHLGDPEPPDSVC



Mon Jan 6 08:48:27 2003

us-09-882-735-2.rge

Page 10

QY	12	1202	AASTHVAALQYSTHYSHSLAQY	PhePheLeuArgIAsnGLUCysVal	140
QY	13	1203	AASTHVAALQYSTHYSHSLAQY	PhePheLeuArgIAsnGLUCysVal	140
DB	66	AAA	AAATAAAGGAGGAGATGATATATAGAGTTT	TAAAGAAAAAGAGTATGTC	146
QY	141	061	CGCGGCAACGCTSYSLYSERLEAGLQYSTHYSLQCYSLQEPGRI	IleGlu	160
DB	14	100	GGAAAGAACTGTAAAGAAAAGG1195AAGACGAAAGTGTGCTTACCCCAATGAG	806	
QY	161	Asn	161		
DB	807	AAAT	809		

Search completed: January 6, 2003, 06:07:28  
Job time : 2835 secs

Downloaded from <http://ajphaphapublications.org/> on 11/01/2017





Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-882-735-2 (1-161) x AAV19801 (1-483)

QY 1 AspSerValCysProGlnGlyTyrIleHisProGlnAsnSerIleCysThr 20  
 DB 1 CATAGTGTCTCTCCCAAGAAATATATCCACCTCAAAATAATTCGATTGCTGACC 60

QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 61 AACTGTCACAAAGAAATCTACTTGTACAAATGACTGTCACAGTCCGGGACAGATACGAC 120

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 121 TCAAGAAATTTGAGAGAGTCTCTTCACTACCTTTACAGAAACACCTTCAGACACTGCTC 180

QY 61 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 181 AGCTGTCCTCAATGCGCAAGCAATGCTCAGGTGGAGATCTCTTCTGCACAGTGGAC 240

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 241 GAGAAATCTCTTAT 300

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 301 TTCTGATGTAATCTGTAAGAAAGCTTGAGTGCAGCAAGTTGTGCTTACCCAGATTGAG 480

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 361 AAAAATAACAAAT 420

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 421 TCCTGATGTAATCTGTAAGAAAGCTTGAGTGCAGCAAGTTGTGCTTACCCAGATTGAG 480

QY 161 Asn 161  
 DB 481 AAT 483

RESULT 3  
 AAV1732  
 ID AAV1732 standard; cDNA; 483 BP.  
 XX AC  
 XX AAV1732;  
 XX 04 MAR 1999 (first entry)  
 XX  
 XX Tumour necrosis inhibitor 30 kDa encoding cDNA.  
 XX  
 XX Tumour necrosis factor receptor 1; TNFR 1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..483  
 FT /\*tag= a  
 FT /note= "no stop codon given"  
 XX  
 XX WC9949305-A1  
 XX  
 XX 05 NOV-1998.  
 XX  
 XX 29-APR-1998; 98WO-US08631.  
 XX  
 XX 01 MAY-1997; 97US-085018A  
 XX  
 XX (AMGEN) AMGEN INC.  
 XX  
 XX Boyle WJ, Wooden S;

XX WPI: 1999-034661/03.  
 DR P-PSDB; AAM89233.  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Disclosure; Fig 2; 92pp; English.

XX The present invention describes a chimeric polypeptide (AI), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated AI monomers; (2) an isolated nucleic  
 CC acid encoding AI; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG dimers  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence encodes the TNF inhibitor 30 kDa protein.

XX SQ Sequence 483 BP; 130 A; 124 C; 123 G; 106 T; 0 other;

Alignment Scores:  
 Pred. No.: 9,46e-79 Length: 483  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US-09-882-735-2 (1-161) x AAV1732 (1-483)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysThr 20  
 DB 1 CATAGTGTCTCTCCCAAGAAATATATCCACCTCAAAATAATTCGATTGCTGACC 60

QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 61 AAGTGCACCAAGAGACCTACTTGTACATGACCTGTCACATTCGGGACAGATACGAC 120

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 121 TGCAGGAGTGTGAGAGCGCTCTTCACTACCTTTACAGAAACACCTTCAGACACTGCTC 180

QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 181 AGCTGTCCTCAATGCGCAAGCAATGCTCAGGTGGAGATCTCTTCTGCACAGTGGAC 240

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 241 CGGACACCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnIleGlu 120  
 DB 301 TTCTGATGTAATCTGTAAGAAAGCTTGAGTGCAGCAAGTTGTGCTTACCCAGATTGAG 480

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 361 AAACAGAACACCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 421 TCCTGATGTAATCTGTAAGAAAGCTTGAGTGCAGCAAGTTGTGCTTACCCAGATTGAG 480

QY 161 Asn 161  
 DB 481 AAT 483

```

RESULT 4
AAC83945
ID AAC83945 standard: DNA; 483 BP.
XX
XX AAC83945;
AC
XX 02-MAR-2001 (first entry)
XX
XX Human 30 kDa TNF inhibitor coding sequence #1.
DE
XX TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
XX IL-1; inflammatory disease; degenerative disease; human; ss.
XX
XX Homo sapiens.
OS
XX US6143866-A.
PN
XX U/-NOV-2000.
PD
XX 19-JAN-1995; 95US-0375242.
PF
XX 19-JUL-1990; 90US-0555274.
PR
XX 09-JUL-1993; 93US-0090366.
PR
XX 18-JUL-1989; 89US-0381080.
PR
XX 11-DEC-1989; 89US-0450329.
PR
XX 07-FEB-1990; 90US-0479661.
XX
XX (AMGEN) AMGEN INC.
XX
XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Varnice J, Kohno T;
XX WPI; 2001-006443/01.
XX P-PSDB; AAB37676.
XX
XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF.
XX
XX Example 6, Fig 20, 82pp; English.
XX
XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
XX (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
XX novel TNF inhibitors of the present invention are useful as therapeutic
XX agents for inhibiting the activity of TNF and interleukin (IL-1), and
XX for treating inflammatory and degenerative diseases mediated by TNF. The
XX present sequence is the coding sequence for the 30 kDa TNF inhibitor
XX The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX
XX Sequence 463 BP, 130 A, 124 C, 123 G, 106 T; 0 other.
SQ

Alignment Scores:
Pred. No.: 9,46e-79 Length: 483
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-882-735-2 (1-161) x AAC83945 (1-483)
QY 1 ApsseVVAICysProGILGILYsTyrILeHsProGILnAsnAsnserILeCysCysThr 20
DB 1 CATAGTGTGTGTGCCCCAAGAAATAATATTCACCCCTAAATAATATTCGATTGTGCTGACC 60
QY 21 LysCysHsILysGILYThrTyrLeuTyrAsnAspCysProGILProGILnAspThrAsp 40
DB 61 AAGTGTCCCAAGAGAACTTACTTGTATATGATGCTTCACGCGCGGCGAGATACGAGAC 120
QY 41 CysATGGLYVYsGILserGILSerPheThrAlaSerGILnAsnHsILeUATGHSILeU 60

```

```

DB 121 TGCAGGAGCTGTGAGACGCGCTCCTTCACCGCTTCAGAAAAACCACTTCAGACATGCTTC 180
QY 61 SerCysSerILysCysArgLYsGluMerGILYGLnValGluILeserSerCysThrValAsp 80
DB 181 AGCTGCTCCAAATGCGCAAGAAAGAAATGGATCAGTGTAGATCTCTTCTTGACAGTGGAC 240
QY 81 ArgAspThrValCysGILYsArgLYsAsnGILnTyrArgHsILeUATGHSILeU 100
DB 241 CGGACACCGCTGTGTGCTGTGCGAGAAAGAACCACTACCGCATATATGAGTAAACCTT 300
QY 101 PheGILnCysPheAsnCysSerLeuCysLeuAsnGILYThrValHsILeUserCysGILnGlu 120
DB 301 TTCAGTCTCTCAATTGACGCTTCTGCTCAATGGAGACCGTGCACCTCTCTGCGACGAGG 360
QY 121 LysGILnAsnThrValCysThrCysHsILaGILYpHePheLeuArgGILnAsnGILYsVal 140
DB 361 AAACAGAAACCGCTGTGCTGACCTGCATGCGAGGTTCTTCTTAAAGAAAAACGATGTGTC 420
QY 141 SerCysSerAsnCysLYsLYsSerLeuGILYsThrLYsLeuCysLeuProGILnILeGILu 160
DB 421 TCTGTAGTAACTGTAAAGAAAGCTGAGTGCACGAAGTGTGCTTACCCAGATTGAG 480
QY 161 Asn 161
DB 481 AAT 483

RESULT 5
AAT94022
ID AAT94022 standard, cDNA; 1301 BP.
XX
XX AAT94022;
AC
XX 19-MAR-1998 (first entry)
XX
XX cDNA for TBP(20-190)/hCG-beta fusion protein.
XX
XX Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
XX beta subunit; hCG-beta; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 279..1289
XX FT
XX W09730161-A1.
XX
XX 21-AUG-1997.
XX
XX 20-FEB-1997; 97MO-US02315.
XX
XX 20-FEB-1996, 96US-0011936.
XX
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX Campbell FK, Chapel SC, Jameson BA;
XX WPI; 1997-425036/39.
XX P-PSDB; AAM33360.
XX
XX Hybrid dimeric protein comprising two co-expressed units - each
XX based on receptor or ligand and a subunit of a heterodimeric
XX hormone, especially FSH, for inducing follicular maturation
XX
XX Example; Pages 39-40; 60pp; English.
XX
XX A novel fusion protein comprises 2 dimer forming co-expressed amino
XX acid sequences, each consisting of a homodimeric or heterodimeric
XX receptor chain or ligand, with ligand-receptor binding activity,
XX bound directly or via a peptide linker to a subunit of a
XX heterodimeric protein hormone capable of forming a heterodimer with
XX the hormone's other subunits. The fusion protein, e.g. the
XX thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
XX

```

CC hCG beta) fusion protein encoded by the present sequence,  
 CC significantly increases the biological activity of the hormone  
 CC component, reducing the requirement for hormone itself and the  
 CC number of injections needed.

XX Sequence 1301 BP; 269 A; 413 C; 351 G; 268 T; 0 other;

## Alignment Scores:

Pred. No.: 3,27e-78 Length: 1301  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 18 Gaps: 0

US-09-882-735-2 (1-161) x AAT94022 (1-1301)

OY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20  
 DB 345 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTTCAAAATATTCGATTTCGTGACC 404  
 OY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 405 AAGTTCGTAAGAAAGAACTATTTATTAATGACTGTCTGAGGCGGGGAGGATACGGAC 464  
 OY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 465 TGAGGTAATTTATGAGTGTCTTCTACAGCTTCAGAAACCACTCAGACACTGCTC 524  
 OY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
 DB 525 AGTGTCTGTAATGAGGTTTAAAGTAAATGATGATGATGATGATGATGATGATGATGAT 584  
 OY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 585 GAGACACCGT 644  
 OY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 645 TTCCAGT 704  
 OY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 705 AAAAT 764  
 OY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 765 TCTGTAT 824  
 OY 161 Asn 161  
 DB 825 AAT 827

## RESULT 6

ID AAQ06282 standard; DNA; 1334 BP.

XX AAQ06282;

XX 29-JAN-1991 (first entry)

XX Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.

XX Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

KW pTNF BP15; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 213..1325

FT /\*tag= a

FT /product=TNF-BP

XX

PN EP393438-A.  
 XX 24-OCT-1990.  
 XX 06-APR-1990; 90EP-0106624.  
 XX 21-JUN-1990; 89DE-3900282.  
 XX 21-APR-1989; 89DE-3913101.  
 XX (BOEH ) BOEHPINGER INGELHEIMINT.  
 PI Hauptmann R, Himmler A, Maurer Foqy I, Stratowa C;  
 XX WPI; 1990-321987/43.  
 DR P-PSDB; AAR07449.  
 XX DNA encoding TNF binding protein and TNF-receptor used in  
 PT tumour treatment and to understand mechanism to TNF action  
 XX Disclosure; Fig 1(1-3); 51pp; German.  
 CC pTNF-BP15 is one of 30 positives clones in a screened cDNA library  
 CC from induced TNF-induced fibrosarcoma cells. A TNF BP had been  
 CC isolated from the urine of patients with uraemia and probes/primers  
 CC were constructed from the determined amino acid sequence.  
 CC To produce a vector expressing a soluble form of TNF binding  
 CC protein, this plasmid was cut with XmnI, amplified by PCR and the  
 CC amplified DNA cut with BamHI and EcoRI.  
 CC The resulting 0.75 kb DNA fragment was inserted into pT7/3 alpha 19  
 CC (BSP) cut with the same enzymes to recover pTNF-BP. This was cut  
 CC with BamHI and EcoRI, and the recovered fragment inserted into  
 CC pAD-CMV1 (AAQ06283) to give the required plasmid pADTNF-BP.  
 CC See also AAQ06282-Q06285.  
 XX Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T; 0 other;

## Alignment Scores:

Pred. No.: 3,38e-78 Length: 1334  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-09-882-735-2 (1-161) x AAQ06282 (1-1334)

OY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20  
 DB 333 GATAGTGTGTGTCCTCCCAAGGAAATATATATATATATATATATATATATATATAT 492  
 OY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 393 AAGTGTCCACAAAGGAACTATTTGTAATGACTGTCTGAGGCGGGGAGGATACGGAC 492  
 OY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 453 TGCAAGGAGTGTGAGAGCGGCTCTTACAGTGTTCAGAAATATATATATATATATAT 612  
 OY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
 DB 513 AGCTGTCCCAATATCCCAAGGAAATATATATATATATATATATATATATATATAT 612  
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 DB 573 CGGACACCGT 612  
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 OY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
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 FT /tag= c  
 FT exon 40..193  
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 FT exon 769..1057  
 FT /tag= o  
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 FT exon 1058..1368  
 FT /tag= p  
 FT /number= 10  
 XX WO2000050436-A1.  
 XX  
 XX 31-AUG-2000.  
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 XX 23 FEB 2000; 2000WO-US04606.  
 XX  
 XX 23 FEB 1999; 99US-0121314.  
 XX  
 XX (GENA) GENA1SSANCE PHARM INC.  
 XX (NAND/) NANDAHALAN K.  
 XX (SCHU/) SCHULZ V P.  
 XX (STEV/) STEPHENS J C.  
 XX (CHEW/) CHEW A.  
 XX  
 XX Nandabalan K, Schulz VP, Stephens JC, Chew A;  
 XX WPI: 2000-543909/49.  
 XX P PSDB; AAB23446.  
 XX  
 XX Polynucleotides comprising polymorphic variants of a reference sequence  
 XX for tumour necrosis factor receptor 1 (TNFR1), useful for studying the  
 XX biological function of TNFR1 and identifying drugs targeting the  
 XX protein for treating disorders -  
 XX  
 XX Claim 7; Fig 4; 79pp; English.  
 XX  
 XX The present invention relates to polymorphic variants of the tumour  
 XX necrosis factor receptor 1 (TNFR1) gene. The present sequence is  
 XX the coding sequence of the TNFR1 gene. The sequence of the whole gene is  
 XX given in AAA95102, AAA95103 and AAA95104. The polymorphisms were  
 XX identified by amplifying and sequencing regions of the gene Twelve

CC polymorphic loci were discovered. Of these twelve polymorphisms, four can  
 CC cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be  
 CC useful for studying the biological function of TNFR1 as well as for  
 CC identifying drugs targeting the protein for treatment of disorders  
 CC related to its abnormal expression or function such as tumours,  
 CC apoptosis related disorders and bacterial infection.  
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 XX SQ Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,496-78 Length: 1368  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-882-735-2 (1-161) x AAA95105 (1-1368)

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 QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 301 AGCTGCTCAAAATGCGAAAGGAAATGAGTCAAGTGTGAGATCTCTTCTTCAACAGTGA 360  
 QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 361 CTGGACACCTGTGTGAGTGTGAGAGGAAAGAACTATGTCATTATTAGTGAACAACTT 420  
 QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnIle 120  
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 QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 481 AAACAGAACACCGTGTGCACCTGCATGCAAGCTTCTTCTTAAAGAGAAACGATATCT 540  
 QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrIleLysLeuCysLeuProGlnIleGlu 160  
 DB 541 TCCTGTAGTAACCTGTAGAGAAAGCTTGAATGACAGAGTTGTGACTAATCAATATGA 600  
 QY 161 Asn 161  
 DB 601 AAT 603

RESULT 9  
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 ID AAX58150 standard; DNA; 1478 BP.  
 XX  
 XX AC AAX58150;  
 XX

DT 21-JUL-1999 (first entry)

DE CadC-fusion polypeptide coding sequence.

KW CadC; fusion protein; tumour necrosis factor alpha interaction domain;  
 KW protein-protein interaction; periplasmic domain; transmembrane domain;  
 KW CadC transcriptional regulatory domain; receptor interaction;  
 KW ligand identification; orphan receptor; ss.

OS Synthetic.

XX WO9923116-A1.













GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd

cM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 04:00:20 : Search time 51 seconds  
(without alignments)

931 603 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQKHYHPQNSICCT CSNCKKSLRCKTKCLPQIEN 161

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Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	941	100.0	1301	4	US-08-804-166-7
3	941	100.0	1301	4	US-08-910-991-7
4	941	100.0	1478	4	US-08-149-922-6
5	941	100.0	2062	2	US-08-050-319B-24
6	941	100.0	2062	2	US-08-465-982-56
7	941	100.0	2161	3	US-09-106-038A-1
8	941	100.0	2161	4	US-09-505-250-3
9	941	100.0	2175	1	US-08-301-668-1
10	941	100.0	2175	1	US-08-837-941-1
11	941	100.0	2175	1	US-08-126-016-1
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13	941	100.0	6889	1	US-08-286-740-2
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15	941	100.0	6896	2	US-08-627-151A-6
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21	842.5	89.5	1049	4	US-08-910-991-1
22	837	88.9	1202	4	US-08-804-166-3
23	837	88.9	1202	4	US-08-910-991-3
24	746	79.3	501	1	US-08-050-319B-1
25	746	79.3	501	2	US-08-465-982-1
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29	731	77.7	372	2	US-08-465-982-3
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32	680	72.3	1956	2	US-08-762-308-10
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40	200.5	21.3	1509	4	US-09-411-722-3
41	200.5	21.3	1634	4	US-08-928-069-11
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44	196	20.8	1438	4	US-08-928-069-5
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## ALIGNMENTS

### RESULT 1

```

US-09-326-394-1
: Sequence 1, Application US/09326394
: Patent No. 6306820
: GENERAL INFORMATION:
: APPLICANT: Bendelle, Alison M.
: APPLICANT: Sennello, Regina M.
: TITLE OF INVENTION: COMBINATION THERAPY USING A TIE BINDING
: TITLE OF INVENTION: PROTEIN FOR TREATING THE MODIFIED DUTAVES
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Inc.
: STREET: 1840 DeHavilland Drive
: CITY: Thousand Oaks
: STATE: CA
: COUNTRY: US
: ZIP: 91320-1789
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1 0, Version #1 30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/326,394
: FILING DATE: 08-DEC-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/032,587
: FILING DATE: 06-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036,355
: FILING DATE: 23 JAN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/039,315
: FILING DATE: 07 FEB-1997

```

Prior Application Data:  
 APPLICATION NUMBER: US 66/052,023  
 FILING DATE: 09-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zindick, Thomas K.  
 REGISTRATION NUMBER: 32,185  
 REFERENCE/DOCKET NUMBER: A-430D  
 INFORMATION FOR SEQ ID NO. 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 483 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..483  
 US-09-326-394-1

Alignment Scores:  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-382-735-2 (1-161) X US-09-326-394-1 (1-483)

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 QY 141 SERCYSSERANCYSLYSLYSEULEUGLUCYSTHRILYSEUCYSLUENPROGINILEGU 160  
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 DB 481 AAT 483

RESULT 2  
 US-08-804-166-7  
 Sequence 7, Application US/08804166  
 Patent No. 6193972  
 GENERAL INFORMATION:  
 APPLICANT: Campbell, Robert K.  
 APPLICANT: Jameson, Bradford A.  
 APPLICANT: Chapel, Scott C.

TITLE OF INVENTION: HYBRID PROTEINS  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/804,166  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/011,936  
 FILING DATE: 20 February 1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Browdy, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: CAMPBELL=2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO. 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1301 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 279..1287  
 US-08-804-166-7

Alignment Scores:  
 Pred. No.: 4,71e-93 Length: 1301  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-882-735-2 (1-161) X US-08-804-166-7 (1-1301)

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 QY 21 LYSYSHISLYSGLYTHRTYRLEUTYRANASPCYSPROGILYPROGILYINAPTHRASP 40  
 DB 405 AAGTCCCAAGAAAGAACTACTGTACATGACTGTCCAGGCCGAGGAGATACCGGAC 464  
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 DB 465 TGCAGGAGTGTGAGAGAGAGTCTTCCACCGCTTCAGAAACCACTTCAACCTGCTC 524  
 QY 61 SERCYSSERLYSCYARGLYSGIUMETGLYINVAIGLIULESERSEYCYSTHRVALASP 80  
 DB 525 AGTGTCTTCAATATGCAAAAGAAATGAGTCAAGTGAATCTCTTCCACAGTGGAC 584  
 QY 81 ARGASPTHVALCYSGLYCYARGLYASNGINTYRARGHISTYRTPSERGIUASNHLEU 100  
 DB 585 CGGACACCGGTGTGCTGCTGAGGAAACCACTACCGGCAATATTTGAGTGAACAACTT 644  
 QY 101 PHEGINSYSPHEASNCYSSEYLEUCYSLUASNGLYTHRVALLHISLEUSERCYSGINGLU 120

Db 645 TTCAGTCTTTAAATGACGCTTGGCTCAATGGGAGCGGTGCACCTCTCTCCAGGAG 704  
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RESULT 3  
US-09-910-991-7  
; Sequence 7, Application US/08910991  
; Patent No. 6194177  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Robert K.  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Chappel, Scott C.  
; TITLE OF INVENTION: HYBRID PROTEINS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street N W , Ste 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22207  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/910,991  
; APPLICATION NUMBER: US/08/910,991  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/804,166  
; FILING DATE: 20 February 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/011,936  
; FILING DATE: 20 February 1996  
; ATTORNEY/AGENT INFORMATION  
; NAME: YUN, Allen C  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/CO-PAT NUMBER: CAMPBELL 2B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628 5197  
; TELEFAX: (202) 737 3528  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1101 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 279..1287  
US-09-910-991-7

Alignment Scores:  
Pred. No.: 4.71e-93 Length: 1301  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-882-735-2 (1-161) x US-08-910-991-7 (1-1301)  
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysValThr 20  
Db 345 GATAGTGTGTGTCCTCCCAAGGAAAATATATATACCTTCAAAATAATTGATTTGAGTAT 404  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 40  
Db 405 AAGTGCACCAAAAGGAACTTACTTTTAATATATATATATATATATATATATATATATAT 464  
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Db 465 TSCAGGAGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCCCTCAATATGATTC 124  
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
Db 525 ASCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGTGGAGATCTCTTTCACACATGAG 140  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 160  
Db 585 CGGACACACCGT 244  
QY 101 PheGlnCysPheAsnSerCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysThr 120  
Db 645 TTTGAGTGTCTTCAATGTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 204  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnThrCysVal 140  
Db 705 AAACAGACACCGT 264  
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
Db 765 TCTTCTATTAATTAAGAGAAAGGCTGAGTGTAAAGAGTTGTCTCAACCCAGATTGAG 824  
QY 161 Asn 161  
Db 825 AAT 827  
RESULT 4  
US-09-149-922-6  
; Sequence 6, Application US/09149922A  
; Patent No. 6265174  
; GENERAL INFORMATION:  
; APPLICANT: Menzel, Polf  
; APPLICANT: Hsing, Weihong  
; APPLICANT: Taggart, Pamela  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING AND MODULATING  
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS  
; FILE REFERENCE: 9366-006  
; CURRENT APPLICATION NUMBER: US/09/149,922A  
; CURRENT FILING DATE: 1998-09-09  
; EARLIER APPLICATION NUMBER: 60/064,058  
; EARLIER FILING DATE: 1997-11-03  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1478  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 58  
; OTHER INFORMATION: n=a, c, g, or t  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 105  
; OTHER INFORMATION: n=a, c, g, or t  
US-09-149-922-6  
Alignment Scores:  
Pred. No.: 5.63e-93 Length: 1478  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 2  
DB: 4 Gaps: 0

US-09-882-735-2 (1-161) x US-09-149-922-6 (1-1478)

QY 1 AspSerValCysProGlnGlyLysThrIleHisProGlnAsnSerIleCysCysThr 20  
DB 941 GATAGTGTGTCCCAAGAAATATATCCACCTCAAAATTAATTCGATTGGTGTAC 1000  
QY 21 LysCysHisSerGlyThrTyLeuThrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 1001 AAAGAGACACCGGCTATTTGTACATATCTGTCAAGGCGCGGCGAGATACGGAC 1060  
QY 41 CysArgGlyCysGlySerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60  
DB 1061 TCCAGGAGATGTGAGAGAGCGGCTTCACCGCTTCAGAAACCCACCTCAGACCTGCTG 1120  
QY 61 SerCysSerLysCysArgGlyGlnMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 1121 AGCTGCTCCAAATCCGAAAGAAATGGGTCAAGGAGATCTCTCTTCGACAGTGGAC 1180  
QY 91 ArgAspThrValCysGlyCysArgGlyAsnGlnIleThrIleGlyIleThrPheSerGlnAsnLeu 100  
DB 1181 GAGAGATAGT 1240  
QY 121 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 1241 HCTGTATTAATTTGAACTTCTGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1300  
QY 141 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140  
DB 1301 AAACAGAACACCGGT 1360  
QY 161 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 1361 TCCGTAGTAACTGTAAAGAAAGCTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1420  
QY 161 Asn 161  
DB 1421 AAT 1423

RESULT 5

US-08-050-319B-24

Sequence 24 Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESS: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/KEY NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

STREET: 635 Bryant Street

TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 2062 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..1519

US-08-050-319B-24

Alignment Scores:

Pred. No.: 8,98e-93

Score: 941.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 1

Gaps: 0

Length: 2062

Matches: 161

Conservative: 0

Mismatches: 0

Indels: 0

US-09-882-735-2 (1-161) x US-08-050-319B-24 (1-2062)

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DB 275 GATAGTGTGTCCCAAGAAATATATCCACCTCAAAATTAATTCGATTGGTGTAC 334

QY 21 LysCysHisSerGlyThrTyLeuThrAsnAspCysProGlyProGlyGlnAspThrAsp 40

DB 335 AAGGCCACAAAGGAACCTGTTGTCATGACTGTCCAGGCCCGGAGAGATACGGAC 394

QY 41 CysArgGlyCysGlySerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60

DB 395 TGCAGGAGATGTGAGAGAGCGCTCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 454

QY 61 SerCysSerLysCysArgGlyGlnMetGlyGlnValGluIleSerSerCysThrValAsp 80

DB 455 AGCTGCTCCAAATCCGAAAGAAATGGGTCAAGGAGATCTCTCTTCGACAGTGGAC 514

QY 81 ArgAspThrValCysGlyCysArgGlyAsnGlnIleThrIleGlyIleThrPheSerGlnAsnLeu 100

DB 515 CGGACACCGGT 574

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120

DB 575 TTCAGTCTTCAATTCGACCTTCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 634

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140

DB 635 AAACAGAACACCGGT 694

QY 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160

DB 695 TCCGTAGTAACTGTAAAGAAAGCTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 754

QY 161 Asn 161

DB 755 AAT 757

RESULT 6

US-08-465-982-24

Sequence 24 Application US/08465982

Patent No. 563786

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESS: Reed & Robbins

STREET: 635 Bryant Street



QY	101	PhgGlyCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	120
Db	6/6	TTTCATGACTTAAATGTAAGTTCTGACTTAATGAGAACTGTAACCTGCTGACAAAG	735
QY	121	LYgGHisAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlyAsnGlyCysVal	140
Db	736	AAATCAAAATACGGTGGACCTGACCTGACAGAGAGGTTTCTTTTAAAGAGAAACCAATGCTGC	795
QY	141	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnHisLeu	160
Db	796	TCTTATGTAATCTTAATAAAAGAGCTGATGTAAGAAATTGTCCTTACCCCAATTGAG	855
QY	161	Asn	161
Db	856	AAAT	858

RESULT 9  
 US-08-321-668-1  
 ? Sequence 1, Application US/08321668  
 ? Patent No. 5665859  
 ? GENERAL INFORMATION:  
 ? APPLICANT: WALLACH, David  
 ? APPLICANT: BRAKEBUSCH, Cord  
 ? APPLICANT: VAREFOLOMEV, Eugene  
 ? APPLICANT: BARKIN, Michael  
 ? TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
 ? TITLE OF INVENTION: THE TGF RECEPTORS, THEIR PREPARATION AND THEIR USE  
 ? NUMBER OF SEQUENCES: 42  
 ? CORRESPONDENCE ADDRES:  
 ? ADDRESSEE: BPOMDY AND HEIMRAY  
 ? STREET: 419 Seventh Street, N.W., Suite 300  
 ? CITY: Washington  
 ? STATE: D.C.  
 ? COUNTRY: USA  
 ? ZIP: 20004  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/321,668

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1

TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1

LENGTH: 2175 base pairs

LENGTH: 2175 base pairs

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STRANDEDNESS: single
;
TOPOLOGY: 1;box
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STRANDEDNESS: single
;
TOPOLOGY: 1;box
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FEATURE.	CDNA
MOLECULE TYPE.	

FEATURE.	CDNA
MOLECULE TYPE.	

NAME/KEY: CDS  
LOCATION: 256-1620NAME/KEY: CDS  
LOCATION: 256-1620

T-000-TFC-00000

T-000-TFC-00000

Fred. No. : 9.67e-93

Fred. No. : 9.67e-93

Percent Similarity: 100.00%

Percent Similarity: 100.00%



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Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US 09 882 735 2 (1 161) x US 08 321 668 1 (1-2175)

QY 1 AspSerValCysProGlnGlyTyrIleHisProGlnAsnAsnSerIleCysCysThr 20
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QY 21 LysCysHisIleGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40
DB 436 AAGTGCACAAAGGAACTTCTTACAACTGTCCAGCCCGGGGAGGATACGGAC 495

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
DB 496 TCCAGGAGTCTTACAGAGTGCTCTTACCGCTTCAGAAACACCACTCAGACACCTGCC 555

QY 61 SerCysSerIleCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 556 AGTGTCTTCAATGCAAGGAAATATATGCTCAGGTGAGATCTCTCTTCACAGTGGAC 615

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 616 CGGACACCGGTGTGCTGCTGACAGAGAAACAGTACCGGATATTGAGTGGAAACCTT 675

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
DB 676 TTCAGTGTCTTCAATGCAAGGAAATATATGCTCAGGTGAGATCTCTCTTCACAGTGGAC 735

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluCysVal 140
DB 736 AAACAGAACCGGTGTGCTGCTGACAGAGAAACAGTACCGGATATTGAGTGGAAACCTT 795

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 796 TCCAGTGTCTTCAATGCAAGGAAATATATGCTCAGGTGAGATCTCTCTTCACAGTGGAC 855

QY 161 Asn 161
DB 856 AAT 858

RESULT 10
US 08 837 941 1
; Sequence 1, Application US/08837941
; Patent No. 5766917
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BPAKERUSCH, Cord
; APPLICANT: VAPPOLOMEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,941
; FILING DATE: 28 APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/321,668
; FILING DATE: 12 OCT 1994
; APPLICATION NUMBER: IL 107268

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; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-837-941-1

Alignment Scores:
Pred. No.: 9,67e-93 Length: 2175
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-882-735-2 (1-161) x US-08-837-941-1 (1-2175)

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QY 21 LysCysHisIleGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40
DB 436 AAGTGCACAAAGGAACTTCTTACAACTGTCCAGCCCGGGGAGGATACGGAC 495

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
DB 496 TCCAGGAGTCTTACAGAGTGCTCTTACCGCTTCAGAAACACCACTCAGACACCTGCC 555

QY 61 SerCysSerIleCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 80
DB 556 AGTGTCTTCAATGCAAGGAAATATATGCTCAGGTGAGATCTCTCTTCACAGTGGAC 615

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 616 CGGACACCGGTGTGCTGCTGACAGAGAAACAGTACCGGATATTGAGTGGAAACCTT 675

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
DB 676 TTCAGTGTCTTCAATGCAAGGAAATATATGCTCAGGTGAGATCTCTCTTCACAGTGGAC 735

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluCysVal 140
DB 736 AAACAGAACCGGTGTGCTGCTGACAGAGAAACAGTACCGGATATTGAGTGGAAACCTT 795

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 796 TCCAGTGTCTTCAATGCAAGGAAATATATGCTCAGGTGAGATCTCTCTTCACAGTGGAC 855

QY 161 Asn 161
DB 856 AAT 858

RESULT 11
US-08-126-016-1
; Sequence 1, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID

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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US 09-882-735-2 (1-161) x US-08-054-970-1 (1-2175)
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QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
DB 436 AAGTGGCAAAAGAACTACTTTACAAATGATGTCTCCAGGCTCCCGGGGACGAGATACCGAC 495
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
DB 496 TCGACGAGTGTGACAGCGGTCTCTCCACCGCTTCAGAAAACCACTTCAGACACTGCTC 555
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 546 ACCTGTCTCAATGCGAAAGGAAATGCTGTCAGGTGGAGATCTCTCTTCACAGTGGAC 615
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 616 CAGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
DB 676 TTTCAATGCTTCAATGCGAAAGGAAATGCTGTCAGGTGGAGATCTCTCTTCACAGTGGAC 735
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 140
DB 736 AAACAGAACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 795
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 796 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 855
QY 161 Asn 161
DB 856 AAT 858
RESULT 13
US 08-286-740-2
; Sequence 2, Application US/08286740
; Patent No. 5561083
; GENERAL INFORMATION:
; APPLICANT: Crowley, Craig W.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
; HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,740
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 798
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6889 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-286-740-2
Alignment Scores:
Pred. No.: 4,87e-92 Length: 6889
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-882-735-2 (1-161) x US 08-286-740-2 (1-6889)
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QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
DB 1785 AAGTGGCAAAAGAACTACTTTACAAATGATGTCTCCAGGCTCCCGGGGACGAGATACCGAC 1844
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
DB 1845 TCGACGAGTGTGACAGCGGTCTCTCCACCGCTTCAGAAAACCACTTCAGACACTGCTC 1904
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 1905 ACCTGTCTCAATGCGAAAGGAAATGCTGTCAGGTGGAGATCTCTCTTCACAGTGGAC 1964
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 1965 CGGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2024
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnIleGlu 120
DB 2025 TTCAGTGTCTTCAATGCGAAAGGAAATGCTGTCAGGTGGAGATCTCTCTTCACAGTGGAC 2084
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 140
DB 2085 AAACAGAACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2144
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 2145 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2204
QY 161 Asn 161
DB 2205 AAT 2207
RESULT 14
PCT-US95-09576-2
; Sequence 2, Application PC/TUS9509576
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH EXPRESSING
; HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 04:00:40 : Search time 273 Seconds  
(without alignments)  
255.067 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941  
Sequence: 1 DSVCPQKHYHPQNSICT ... CSNCKSLETKLIPQIEN 161

Scoring table: RLSUM62

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Ygapop 10 0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 181593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40 codi -LIST=45 -DOCALIGN=200 -THP SCOPE=PCT -THP MAX=100  
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NUPY=6 -ICPU=3 -NO\_XLPHY -NO\_WMAP -LAPGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
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Database :

Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	100.0	483	9	US-09-898-234-3 Sequence 3, Appli
2	941	100.0	483	9	US-09-899-429A-3 Sequence 3, Appli
3	941	100.0	483	9	US-09-792-356-3 Sequence 3, Appli
4	941	100.0	483	10	US-09-899-429-3 Sequence 3, Appli

5	941	100.0	483	10	US-09-907-263-1 Sequence 1, Appli
6	941	100.0	486	9	US-09-899-429A-5 Sequence 5, Appli
7	941	100.0	516	9	US-09-899-429A-19 Sequence 19, Appli
8	941	100.0	519	9	US-09-899-429A-15 Sequence 15, Appli
9	941	100.0	549	9	US-09-899-429A-9 Sequence 9, Appli
10	941	100.0	579	9	US-09-899-429A-17 Sequence 17, Appli
11	941	100.0	609	9	US-09-899-429A-11 Sequence 11, Appli
12	941	100.0	603	9	US-09-899-429A-13 Sequence 13, Appli
13	941	100.0	633	9	US-09-899-429A-7 Sequence 7, Appli
14	941	100.0	1301	10	US-09-756-186-7 Sequence 7, Appli
15	941	100.0	1334	9	US-09-898-234-11 Sequence 11, Appli
16	941	100.0	1334	9	US-09-792-356-11 Sequence 11, Appli
17	941	100.0	1334	10	US-09-899-422-11 Sequence 11, Appli
18	941	100.0	1368	9	US-09-898-234-1 Sequence 1, Appli
19	941	100.0	1368	9	US-09-899-429A-1 Sequence 1, Appli
20	941	100.0	1368	9	US-09-792-356-1 Sequence 1, Appli
21	941	100.0	1368	10	US-09-899-422-1 Sequence 1, Appli
22	941	100.0	2111	10	US-09-880-157-2360 Sequence 2360, Ap
23	941	100.0	2141	9	US-09-898-234-16 Sequence 16, Appli
24	941	100.0	2141	9	US-09-899-429A-26 Sequence 26, Appli
25	941	100.0	2141	9	US-09-792-356-16 Sequence 16, Appli
26	941	100.0	2141	10	US-09-899-422-16 Sequence 16, Appli
27	941	100.0	2175	12	US-10-120-397-1 Sequence 1, Appli
28	931	98.9	1334	9	US-09-899-429A-21 Sequence 21, Appli
29	928	98.6	1147	10	US-09-756-186-5 Sequence 5, Appli
30	842.5	89.5	1049	10	US-09-756-186-1 Sequence 1, Appli
31	837	88.9	1263	10	US-09-756-186-3 Sequence 3, Appli
32	680	72.3	5870	10	US-09-838-718A-8 Sequence 8, Appli
33	674.5	71.7	543	10	US-09-970-532-3 Sequence 3, Appli
34	674.5	71.7	2440	10	US-09-970-532-1 Sequence 1, Appli
35	669	71.1	2130	10	US-09-917-800A-1601 Sequence 1601, Ap
36	656	69.7	2173	9	US-09-898-234-14 Sequence 14, Appli
37	656	69.7	2173	9	US-09-899-429A-24 Sequence 24, Appli
38	656	69.7	2173	9	US-09-792-356-14 Sequence 14, Appli
39	656	69.7	2173	10	US-09-899-422-14 Sequence 14, Appli
40	293	31.1	158	9	US-09-898-234-68 Sequence 68, Appli
41	293	31.1	158	9	US-09-792-356-68 Sequence 68, Appli
42	293	31.1	158	10	US-09-899-422-68 Sequence 68, Appli
43	273	29.0	158	9	US-09-899-429A-78 Sequence 78, Appli
44	255.5	27.2	151	9	US-09-938-234-29 Sequence 29, Appli
45	255.5	27.2	151	9	US-09-899-429A-30 Sequence 30, Appli

ALIGNMENTS

RESULT 1  
US-09-898-234-3  
; Sequence 3, Application US/09898234  
; Patent No. US20020155112A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-1  
; CURRENT APPLICATION NUMBER: US/09/898,234  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,410  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 483

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(483)  
US-09-898-234-3

## Alignment Scores:

Pred. No.	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3,22e-94	483	161	0	0	0	0
Score:	941.00	100.00%	100.00%	100.00%	100.00%	100.00%
Best Local Similarity:	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%
Query Match:	9	0	0	0	0	0

US-09-882-735-2 (1-161) x US-09-898-234-3 (1-483)

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Cv 1  AASPserValCysProGlnGlySerThrValLeuHisProGlnAsnAsnSerIleCysCysThr 20
Db 1  GATAGTGTGTGTCCCAAGGAAATATATCCACCTTCAAAATATATGATTTGCTGTACC 60
Cv 21  LysCysHisLysGlyThrThrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
Db 61  AAGTGTATCAAAAGAAACCTACTTGTATATATCTTGTCAAGTCCGAGGATACCGAC 120
Cv 41  CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db 121  TGAAGGAAATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Cv 61  SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
Db 181  AATTGTCTCAATATATATATATATATATATATATATATATATATATATATATATAT 240
Cv 81  ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 100
Db 241  CCGGACACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Cv 101  PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 301  TTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Cv 121  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140
Db 361  AAGAGAAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Cv 141  SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGln 160
Db 421  TCCGTAGTAACTTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Cv 161  Asn 161
Db 481  AAT 483

```

## RESULT 2

US-09-899-429A-3

Sequence 3, Application US/09899429A  
Parent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIORITY APPLICATION NUMBER: 09/794,356  
PRIORITY FILING DATE: 2000-02-03  
PRIORITY APPLICATION NUMBER: 08/477,639  
PRIORITY FILING DATE: 1995-06-07  
PRIORITY APPLICATION NUMBER: 08/383,676  
PRIORITY FILING DATE: 1995-02-01

PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 3  
LENGTH: 483  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(483)  
US-09-899-429A-3

## Alignment Scores:

Pred. No.	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3,22e-94	483	161	0	0	0	0
Score:	941.00	100.00%	100.00%	100.00%	100.00%	100.00%
Best Local Similarity:	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%
Query Match:	9	0	0	0	0	0

US-09-882-735-2 (1-161) x US-09-899-429A-3 (1-483)

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Cv 1  AASPserValCysProGlnGlySerThrValLeuHisProGlnAsnAsnSerIleCysCysThr 20
Db 1  GATAGTGTGTGTCCCAAGGAAATATATCCACCTTCAAAATATATGATTTGCTGTACC 60
Cv 21  LysCysHisLysGlyThrThrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
Db 61  AAGTGTATCAAAAGAAACCTACTTGTATATATCTTGTCAAGTCCGAGGATACCGAC 120
Cv 41  CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db 121  TGAAGGAAATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Cv 61  SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
Db 181  AAGTGTATCAAAAGAAACCTACTTGTATATATCTTGTCAAGTCCGAGGATACCGAC 240
Cv 81  ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 100
Db 241  CCGGACACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Cv 101  PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 301  TTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Cv 121  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140
Db 361  AAGAGAAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Cv 141  SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGln 160
Db 421  TCCGTAGTAACTTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Cv 161  Asn 161
Db 481  AAT 483

```

## RESULT 3

US-09-792-356-3

Sequence 3, Application US/09792356  
Publication No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for





DB 421 TCGTGTAGTAACTGTAAAGAAAGCTGAGTGCAGAAATTGTGTCTTACCCCAATTGAG 480  
 CY 161 Asn 161  
 DB 481 AAT 483

## RESULT 5

US-09-907-263-1  
 Sequence 1, Application US/09907263  
 Patent No. US20020192241  
 GENERAL INFORMATION:  
 APPLICANT: Bendelle, Alison M.  
 Sennello, Regina M.  
 Edwards, Carl K.

TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
 PROTEIN FOR TREATING TNF-MEDIATED DISEASES

NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
 STREET: 1840 DeHavilland Drive  
 CITY: Thousand Oaks  
 STATE: CA

COUNTRY: US  
 ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/907,263  
 FILING DATE: 17-Jul-2001

CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/326,334  
 FILING DATE: 1999-06-04  
 APPLICATION NUMBER: US 60/036,355  
 FILING DATE: 23-JAN-1997  
 APPLICATION NUMBER: US 60/039,315  
 FILING DATE: 07-FEB-1997  
 APPLICATION NUMBER: US 60/052,023  
 FILING DATE: 09-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zindrick, Thomas K.  
 REGISTRATION NUMBER: 32,185  
 REFERENCE/DOCKET NUMBER: A-4300

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 483 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..483  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-907-263-1

## Alignment Scores:

Pred. No.: 3,22e-94 Length: 483  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conserved: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-899-725-2 (1..161) X US-09-907-263-1 (1..483)

CY 1 AggSerValGysProGlnGlyLysTyrLleHisProGlnAsnAsnserLleGysCysThr 20  
 DB 1 GATGAGTGGTGGCCCAAGGAAATATATTCACCCCTCAAAATATATTCGATTTCGTGACC 60

CY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnGlnAspThrAsp 40  
 DB 61 AAGTGCACCAAGAGACCTTACTGTACAAATGACTGTCCAGGCCCC333AGATACGAC 120  
 CY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60  
 DB 121 TCGAGGAGTGGAGAGGGGCTCTTACCGCTTCAGAAACCACTTCAGACACTGCTTC 180  
 CY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
 DB 181 AGCTGCTCCAAATCCCAAGAAAGAAATGGTCAAGTGAAGATCTCTTCTTGACACAGTGGAC 240  
 CY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 241 CGGACACCGGTGTGTGCTGTGAGAAACACAGATACCGGATATTTGAGTGAACCTT 300  
 CY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 301 TTCAGTCTTCAATTGCGAGCTCTGCTCAATGGAGACCTGCTCTGCGCAGAG 360  
 CY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140  
 DB 361 AAACAGAACACCGTGTGACCTGCGCATGCGAGGTTTCTTTCTTAAGAGAAACAGAGTGTGTC 420  
 CY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 421 TCTGTAGTAACTGTAAAGAAAGCTGAGTGCAGCAAGTTGTGCTTACCCCAATTGAG 480  
 CY 161 Asn 161  
 DB 481 AAT 483

## RESULT 6

US-09-899-429A-5  
 Sequence 5, Application US/09899429A  
 Patent No. US20020169118A1  
 GENERAL INFORMATION:

APPLICANT: Hauptmann, Rudolph  
 APPlicant: Himmler, Adolph  
 APPlicant: Maurer-Peggy, Ingrid  
 TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 FILE REFERENCE: 98-385-J  
 CURRENT APPLICATION NUMBER: US/09/899,429A  
 CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: 09/792,356  
 PRIOR FILING DATE: 2000-02-23  
 PRIOR APPLICATION NUMBER: 08/477,639  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: 08/383,676  
 PRIOR FILING DATE: 1995-02-01  
 PRIOR APPLICATION NUMBER: 08/153,287  
 PRIOR FILING DATE: 1993-11-17  
 PRIOR APPLICATION NUMBER: 07/821,750  
 PRIOR FILING DATE: 1992-01-02  
 PRIOR APPLICATION NUMBER: 07/511,430  
 PRIOR FILING DATE: 1990-04-20

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 486

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: recombinant

NAME/KEY: CDS

LOCATION: (1)..(486)

US-09-899-429A-5

Alignment Scores: 3,25e-94 Length: 486

Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-882-735-2 (1-161) x US-09-899-429A-5 (1-486)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
DB 4 CATAGTGTGTGTCCTCCAGGAAATATATATCCCTCAAAATAATTCGATTTCTGTACC 63  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 40  
DB 64 AAGTGTCCAAAGGAAACCTATTCTACAACTGCTCCAGGCGGCGGAGGATACGGAC 123  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 124 TGACAGAGTGTGAGAGGAGTCTCTTCCAGGCTTCAGAAAACCACTCAGACACTGCTC 183  
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 184 AGCTGCTCAATGCGGAAAGAAATGAGTCTGAGATCTCTTCTGACAGTGGAC 243  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
DB 244 TGGATACCTGT 303  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 304 TTTGATGCTTAAATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 363  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 364 AAACAGAACAGT 423  
QY 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 424 TCTGTATATTAATTTAAAGAAAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 483  
QY 161 Asn 161  
DB 484 AAT 486

## RESULT 7

US-09-899-429A-19  
Sequence 19, Application US/09899429A  
Patent No. US20020169118A1

## GENERAL INFORMATION:

APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09899429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,297  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 19

LENGTH: 516  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
NAME/KEY: CDS  
LOCATION: (1)..(516)  
US-09-899-429A-19

Alignment Scores:  
Pred. No.: 3,54e-94 Length: 516  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-882-735-2 (1-161) x US-09-899-429A-19 (1-516)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
DB 4 CATAGTGTGTGTCCTCCAGGAAATATATATCCCTCAAAATAATTCGATTTCTGTACC 64  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 40  
DB 64 AAGTGTCCAAAGGAAACCTATTCTACAACTGCTCCAGGCGGCGGAGGATACGGAC 124  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 124 TGACAGAGTGTGAGAGGAGTCTCTTCCAGGCTTCAGAAAACCACTCAGACACTGCTC 184  
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 184 AGCTGCTCAATGCGGAAAGAAATGAGTCTGAGATCTCTTCTGACAGTGGAC 244  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
DB 244 TGGATACCTGT 304  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 304 TTTGATGCTTAAATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 364  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 364 AAACAGAACAGT 424  
QY 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 424 TCTGTATATTAATTTAAAGAAAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 484  
QY 161 Asn 161  
DB 484 AAT 486

## RESULT 8

US-09-899-429A-15  
Sequence 15, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09899429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639

RESULT 9  
 US-09-899-429A-9  
 Sequence 9, Application US/0909429A  
 Patent No. US7001691B1  
 GENERAL INFORMATION:

Cy	1	AspSerValCysProGlnGluLysTyrThrIleHisProGlnAsnAspSerIleCysLeuThr	20
Dh	37	GATAAGTGTGTGTCCCAAGAGAAATATATACACCTCCAAATAATGCATTTGTTGTAAC	96
Cy	21	LysCysHisLysGlyThrTyrLeuValAspAspCysProGluGluLaseThrAsp	40
Dh	97	AAGTGTGCAAAAGAGAACTATTGTTCATAATGATTTTCAGGCGCGGAGGATACCGAC	156
Cy	41	CysAGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	60
Dh	157	TGTAAGAGTGTGAACAGCGCTGCTTCACAGCTTACGAAACACCTGACATCTGCTGTC	216
Cy	61	SerCysSerLysCysArgLysIleMerGluValGluIleSerSerCysThrValAsp	80
Dh	217	AGTGTGTCGAAATGCGGAAAGAGAAATGCGAGGTGAGATATCTTTCTTGACAGTGGAC	276
Cy	81	ArgAspThrValTyrGlyCysArgCysAsnIleTyrArgHisTyrTrpSerGluAsnLeu	100
Dh	277	CGGACATCGTGTGTGGCTTGCAGCAAAACATACCTGCGCATTTATTTGAGAGAAACCTT	336
Cy	101	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	120
Dh	337	TTTCACATGTTTAAATTTAGCGCTTTGTGCTTAAAGGACCGTGAACCTCTCTGCACAGAG	396
Cy	121	LysGluAsnThrValCysThrCysHisLalaGluPhePheLeuArgLAsnGluCysVal	140
Dh	397	AAACCAAAATACGCTGTGTACCTTGCATATGCAAGTCTTTCTTTTAAAGAGAAACGATGTGTC	456
Cy	141	SerCysSerAsnCysValLysSerLeuGluCysThrLysLeuCysLeuProGluHisLeu	160

DB 457 TCCCTATTAACGTGAAGAAAAAGCCTGGAGTGCACGAAGATTGTGCTACCCAGATTGAG 516  
|||  
QY 161 Asn 161  
|||  
DB 517 AAT 519  
|||  
RESULT 10  
US-09-899-429A-17  
; Sequence 17, Application US/09899429A  
; Patent No. US20020169118A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Hammler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; TITLE OF INVENTION: Them  
; FILE REFERENCE: 98-385-J  
; CURRENT APPLICATION NUMBER: US/09/899,429A  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/792,356  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 08/477,639  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patent In Ver 2.0  
; SEQ ID NO 17  
; LENGTH: 570  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recombinant  
; OTHER INFORMATION: TNF-BP sequence  
; NAME/KEY: CDS  
; LOCATION: (1)..(570)  
US-09-899-429A-17  
Alignment Scores:  
Pred. No.: Length: 570  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-882-735-2 (1-161) x US-09-899-429A-17 (1-570)  
QY 1 AspSerValCysProGlnGlyThrTyrIleHisProGlnAsnSerIleCysCysThr 20  
DB 88 GATACGTGTGTCTTCAAGAAAAATATATCCACCTCAAAAATAATTCGATTTCGTGACC 147  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 148 AATCTCTATAAAATAAATTAATTTATACAAATATATCTCTACAGCCCTCCAGATACGAGAC 207  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 204 TTTACAGCACTTTTACAGAGGTTTCTTACCTTCAGAAAACCCACCTCAGACACTGCTC 267  
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 268 AGCTCTTCAAACTCTTAAATGAGTCTAGTGGAGATCTTTCTTTCACAGTGTAC 327  
QY 81 AspAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100

DB 358 CGGACACCGGTGTGTCTGCTCCAGGAAACAACTATACGCTATATATATATATATAT 487  
|||  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysThrIle 120  
|||  
DB 388 TTCAGTGCCTCAATTGCAAGTGTCTTAAATGAGAGCTTCAATCTCTCTCTCTCTCTCT 447  
|||  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlyVal 140  
|||  
DB 448 AAACAGAACACCGTGTGCACCTGCTCATGTCAGGTTTCTTTCTAAGATGAAATGATG 507  
|||  
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrThrLysLeuCysLeuProGlnIle 160  
|||  
DB 508 TCTTCTATACTTAAATAAAAGGCTGTAATCTGTAAGAAATTTGTGCTATATCTAA 567  
|||  
QY 161 Asn 161  
|||  
DB 568 AAT 570  
|||  
RESULT 11  
US-09-899-429A-11  
; Sequence 11, Application US/09899429A  
; Patent No. US20020169118A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Hammler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; TITLE OF INVENTION: Them  
; FILE REFERENCE: 98-385-J  
; CURRENT APPLICATION NUMBER: US/09/899,429A  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/792,356  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 08/477,639  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,430  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patent In Ver 2.0  
; SEQ ID NO 11  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recombinant  
; OTHER INFORMATION: TNF-BP sequence  
; NAME/KEY: CDS  
; LOCATION: (1)..(600)  
US-09-899-429A-11  
Alignment Scores:  
Pred. No.: Length: 600  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-882-735-2 (1-161) x US-09-899-429A-11 (1-600)  
QY 1 AspSerValCysProGlnGlyThrTyrIleHisProGlnAsnSerIleCysCysThr 20  
DB 88 GATACGTGTGTCTTCAAGAAAAATATATATATATATATATATATATATATATATAT 147  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40

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Db      144  AAHSGCWAAMAAAGVATATITTAATACATGTCACGCGCGGACAGATACGAGAC 207
Q7      41  CysArgGluGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db      208  TCGAGGAACTTGAAGAGAGAGTCTTACGCGCTTAAAGAAACGACCTTACACATCTGCTT 267
Q7      41  SerCysSerLysCysArgLysGluMetGlyGlnValIleSerSerCysThrValAsp 80
Db      268  AATTATCTTAATTCGCGAAAGAAATGCGATGCGATGCGATCTCTTCTTGACACGTGAC 327
Q7      89  AAGAGCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 100
Db      328  GCGAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 387
Q7      121  PheGlnCysPheAsnGlySerLeuGlySerLeuGlyThrValHisLeuSerCysGlnGlu 120
Db      388  TCGAGGAACTTGAAGAGAGAGTCTTACGCGCTTAAAGAAACGACCTTACACATCTGCTT 447
Q7      141  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db      448  AAAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 507
Q7      141  SerCysSerLysCysArgLysGluMetGlyGlnValIleSerSerCysThrValAsp 160
Db      508  TCGAGGAACTTGAAGAGAGAGTCTTACGCGCTTAAAGAAACGACCTTACACATCTGCTT 567
Q7      161  Asn 161
Db      568  AAT 570

RESULT 12
US-09-899-429A-13
Sequence 13, Application US/09899429A
Patent No. US20020169118A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hummel, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98-385-J
CURRENT APPLICATION NUMBER: US/09/899-429A
CURRENT FILING DATE: 2001-07-03
PRIORITY FILING DATE: 1999-02-23
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1995-02-01
PRIORITY FILING DATE: 1993-11-17
PRIORITY FILING DATE: 1992-01-02
PRIORITY FILING DATE: 1992-01-02
PRIORITY FILING DATE: 1990-04-29
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 603
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recombinant
OTHER INFORMATION: TNF-RP sequence
NAME/KEY: CDS
LOCATION: (1)-(603)
US-09-899-429A-13

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Alignment Scores: 4.42e-94 Length: 603  
 Pred. No.: 941.00 Matches: 161  
 Score: 161

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-899-735-2 (1-161) X US-09-899-429A-13 (1-603)

Q7      1  AspSerValCysProGlnGlyLysTyrIleHisPheGlnAsnAsnSerIleCysCysThr 20
Db      121  GATAGTGCTGCCCAAGGAAATATATATCCACCTCAAAATATATGATTCGTCTTAC 180
Q7      21  LysCysHisLysGlyTyrTyrIleCysAsnAspCysPheGlyPheGlyHisLeuPhe 40
Db      181  AAGTGCACAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Q7      41  CysArgGluGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db      241  TGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Q7      61  SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
Db      301  AGTGTCTTAATTCGCGAAAGAAATGCGATGCGATGCGATCTCTTCTTGACACGTGAC 360
Q7      81  ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrPheGluAsnLeu 100
Db      361  CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Q7      101  PheGlnCysPheAsnGlySerLeuGlySerLeuGlyThrValHisLeuSerCysGlnGlu 120
Db      421  TCGAGGAACTTGAAGAGAGAGTCTTACGCGCTTAAAGAAACGACCTTACACATCTGCTT 480
Q7      121  LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db      481  AAAAGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Q7      141  SerCysSerLysCysArgLysGluMetGlyGlnValIleSerSerCysThrValAsp 160
Db      541  TCGAGGAACTTGAAGAGAGAGTCTTACGCGCTTAAAGAAACGACCTTACACATCTGCTT 600
Q7      161  Asn 161
Db      601  AAT 603

RESULT 13
US-09-899-429A-7
Sequence 7, Application US/09899429A
Patent No. US20020169118A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Hummel, Adolph
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98-385-J
CURRENT APPLICATION NUMBER: US/09/899-429A
CURRENT FILING DATE: 2001-07-03
PRIORITY FILING DATE: 1999-02-23
PRIORITY FILING DATE: 1999-02-23
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1995-02-01
PRIORITY FILING DATE: 1993-11-17
PRIORITY FILING DATE: 1992-01-02
PRIORITY FILING DATE: 1992-01-02
PRIORITY FILING DATE: 1990-04-29
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 603

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-RP sequence
; NAME/KEY: CDS
; LOCATION: (1)..(633)
US-09-899-429A-7

Alignment Scores:
Pred. No.: 4,74e-94 Length: 633
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-882-735-2 (1-161) x US-09-899-429A-7 (1-633)
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAnAsnSerIleCysCysThr 20
DB 121 GATATGTCGTCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTGCTGACC 180
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
DB 181 AAGTCGCCAACAAGAACCTACTTGTACAAATGACTGTCCAGGCGCGGCGGATACGGAC 240
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
DB 241 TGCAGGAGTGTGATGAGTGGTCTTCCCGCTTCAGAAACACCTCCAGACACTGGCTC 300
QY 61 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 301 AGTGTGTCCTCAATATGCAAGTAAATGATGTCAGGTGAGATCTTCTTGCACAGTGGAC 360
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 361 CGGAAACAAATGATGTCATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGAACCTT 420
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
DB 421 TTCTGATGTTAAATGAGCTTTCGCTCAATGGACCGTGCACCTCTCTGCCAGGAG 480
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
DB 481 AAAAACAATGATGTCATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGAACCTT 540
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 541 TCTTGATGTTAAATGAGCTTTCGCTCAATGGACCGTGCACCTCTCTGCCAGGAG 600

QY 161 Asn 161
DB 601 AAT 603

RESULT 14
US-09-756-186-7
; Sequence 76, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO. 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 279..1287
US-09-756-186-7

Alignment Scores:
Pred. No.: 1.33e-93 Length: 1301
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-882-735-2 (1-161) x US-09-756-186-7 (1-1301)
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAnAsnSerIleCysCysThr 20
DB 345 GATATGTCGTCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTGCTGACC 404
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
DB 405 AAGTCGCCAACAAGAACCTACTTGTACAAATGATGTCAGGTGAGATCTTCTTGCACAGTGGAC 464
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysVal 60
DB 465 TGCAGGAGTGTGAGAGCGGTCTTCTTCCCGCTTCAGAAACACCTCCAGACACTGGCTC 624
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 525 AGTGTGTCCTCAATATGCAAGTAAATGATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGAACCTT 584
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 585 CGGCAACACCGTGTGTCAGTGGTCTTCAATGGACCGTGCACCTCTCTGCCAGGAG 644
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
DB 645 TTCAGTGTCTTCAATATGCAAGTAAATGATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGAACCTT 704
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
DB 705 AAACAGAACACCGTGTGTCAGTGGTCTTCAATGGACCGTGCACCTCTCTGCCAGGAG 764
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 765 TCTTGATGTTAAATGAGCTTTCGCTCAATGGACCGTGCACCTCTCTGCCAGGAG 824

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CY 161 Asn 161  
DB 825 AAT 827

## RESULT 15

US-09-898-234-11

Sequence 11, Application US/09898234  
Patent No. US2002015112A1  
GENERAL INFORMATION  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummel, Adolph  
APPLICANT: Maurer-Pegz, Ingrid  
APPLICANT: Strietow, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98/385-1  
CURRENT APPLICATION NUMBER: US/09/898,234  
CURRENT FILING DATE: 2001-07-03  
PRIORITY APPLICATION NUMBER: 99/525,998  
PRIORITY FILING DATE: 2000-03-15  
PRIORITY APPLICATION NUMBER: 98/383,676  
PRIORITY FILING DATE: 1995-02-01  
PRIORITY APPLICATION NUMBER: 08/153,287  
PRIORITY FILING DATE: 1993-11-17  
PRIORITY APPLICATION NUMBER: 07/622,750  
PRIORITY FILING DATE: 1992-01-02  
PRIORITY APPLICATION NUMBER: 07/511,430  
PRIORITY FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11  
LENGTH: 1334  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1231..(1325)  
OTHER INFORMATION: Description of Artificial Sequence: CDNA insert of  
OTHER INFORMATION: Lambda-TNF ERI5 and pTNF-BP15 vectors  
US-09-898-234-11

## Alignment Scores:

Pred. No.: 1,38e-93 Length: 1334  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-882-735-2 (1-161) x US-09-898-234-11 (1-1334)

CY 1 ASDSCVMAICSPYSGINQIlyserTTLLeHSPGCIASLAsnSerIleCysCysThr 20  
DB 333 GATAGTGTGTGTCCTCAAGAAATATATCCACCTCAAAATATATGATTGCTGACC 392  
CY 21 LysGlnAsnThrValCysThrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 333 AAAGTGTGTGTCCTCAAGAAATATATCCACCTCAAAATATATGATTGCTGACC 392  
CY 41 CysATGSLVCGSLVserGILserPheThrAlAserGluAsnHisLeuArgHisCysLeu 60  
DB 463 TCGATGATGTGTGTCCTCAAGAAATATATCCACCTCAAAATATATGATTGCTGACC 392  
CY 61 SerCysSerAsnCysLysGlnGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
DB 513 AAGTGTGTGTGTCCTCAAGAAATATATCCACCTCAAAATATATGATTGCTGACC 392  
CY 81 ArgAsnThrValCysSerCysLysGlnGluMetGlyGlnValGlnIleSerSerCysThrValAsnLeu 100  
DB 513 AAGTGTGTGTGTCCTCAAGAAATATATCCACCTCAAAATATATGATTGCTGACC 392  
CY 121 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120

DB 633 ITCCAGTCTTCCAAATGAGGCTTTCCTCAAGGAGCGGTCACCTCTCTCCGACGAG 692  
CY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 693 AAACGAAACACCGTGTGACCTGCGCATGCGAGTTTCTTCTTAAGAGAAAACGAGTGTTC 752  
CY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrIleCysLeuCysLeuProGlnIleGlu 160  
DB 753 TCGATGATGTGTGTCCTCAAGAAATATATCCACCTCAAAATATATGATTGCTGACC 392  
CY 161 Asn 161  
DB 813 AAT 815

Search completed: January 6, 2003, 04:13:57  
Job time : 281 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame plus p2n model

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Run on: January 6, 2003, 04:09:21 , Search time 2190 Seconds
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        1190.627 Million cell updates/sec
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Title: US-09-882-735-2  
Perfect score: 941  
Sequence: 1 DSVCPQGYTHPNNSIGCT ..... CSNCKSECTKCLCPQEN 161

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Ygapop	10.0	Ygapext 0.5
Fgapop	6.0	Fgapext 7.0
Delop	6.0	Delext 7.0

Searched: 16154066 seqs. 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DP seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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UNITS=bits -START=1 -ENDP=1 -MATRIX=BLOSUM62 -TRANS=human40.cd1 -LIST=45
DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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ucp-hisgaap2745.acfn.1.1.763/runat_03012003_074146_17227-HICPU=6 -ICPU=3
NO XIPXY NO MMAP -LARGQUERY NEG SCORES=0 -WAIT -LOGLOG DEV TIMEOUT=120
WARN TIMEOUT=30 -THRPAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
YGAFCP=10 YGAEXT=0 5 DELOP=6 DELEXT=7
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Database : EST.*
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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: qb_est1.*
10: qb_est2:*
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12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
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17: qb_gss:*
18: em_gss_hun
19: em_gss_inr
20: em_gss_pla
21: em_gss_vit
22: em_gss_fun
23: em_gss_mau
24: em_gss_mu
25: em_gss_oth
26: em_gss_pre
27: em_gss_ro

```

ppred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
C	1	941	100.0	931	14	E0723672	BO723672 A-BEN-CURT
	2	941	100.0	957	9	AL559050	AL559050 AL559050
	3	941	100.0	974	12	EG180101	EG180101 602429626
	4	937	99.6	761	9	AU131978	AU131978 AU131978
	5	932	99.0	837	9	AL522988	AL522988 AL522988
	6	931	98.9	1070	13	BM546826	BM546826 A-BEN-CURT
	7	917	97.4	994	14	BM800044	BM800044 A-BEN-CURT
	8	908	96.5	818	13	FA7421169	FA7421169 6040-5008
	9	903	96.0	975	9	AL577008	AL577008 AL577008
	10	892	94.8	859	13	BI870917	BI870917 603394462
	11	888	94.4	942	9	AL529836	AL529836 AL529836
	12	888	94.4	969	12	BE871809	BE871809 601448388
	13	868	92.2	872	13	BI769006	BI769006 6040-8164
	14	864	91.8	845	9	AU125021	AU125021 AU125021
	15	859.5	91.3	916	13	BI757305	BI757305 604029619
	16	848	90.1	859	9	AU124446	AU124446 AU124446
C	17	846	89.9	767	9	AU142156	AU142156 AU142156
	18	844	89.7	872	14	BQ723589	BQ723589 A-BEN-CURT
	19	832.5	88.5	1008	14	BQ719773	BQ719773 A-BEN-CURT
	20	817	86.8	772	9	AU137990	AU137990 AU137990
	21	816.5	86.8	971	12	BR876920	BR876920 601488490
	22	815.5	86.7	823	13	BI766980	BI766980 604054066
	23	815	86.6	936	12	BG681438	BG681438 602624108
	24	793	84.3	951	14	BQ882784	BQ882784 A-BEN-CURT
	25	792	84.2	475	12	BE710028	BE710028 ILA HT001
	26	790.5	94.0	959	12	EG677312	EG677312 602623792
	27	785	83.4	817	9	AU125680	AU125680 AU125680
	28	781	83.0	913	14	BQ226429	BQ226429 A-BEN-CURT
	29	771	81.9	712	10	BE549214	BE549214 601098765
	30	763	81.1	846	13	BI917624	BI917624 603183744
	31	757	80.4	706	9	AU124156	AU124156 AU124156
	C	32	737	78.3	934	13	RI831497
33		728	77.4	387	14	BQ335492	BQ335492 PM4 MTC43
34		727	77.3	834	9	AU126303	AU126303 AU126303
35		718	76.3	415	12	BG001080	BG001080 QV1 GND20
36		713	75.8	822	13	BI260829	BI260829 602971043
37		711	75.6	491	12	BF839822	BF839822 EG3 H1023
38		708	75.2	826	13	BI727271	BI727271 604094399
39		696	74.0	788	9	AU124519	AU124519 AU124519
40		692	73.5	802	9	AU142163	AU142163 AU142163
41		691.5	73.5	805	9	AU125694	AU125694 AU125694
42		684	72.7	761	12	BG582718	BG582718 604060578
43		680	72.3	775	13	BF555040	BF555040 604036950
44		680	72.4	779	9	AU119338	AU119338 ut0400439
45		679	72.2	735	12	BG963025	BG963025 602790349

## ALIGNMENTS

RESULT 1  
BQ723672  
LOCUS  
DEFINITION  
ACCESSION  
BQ723672  
BQ723672  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 931)  
NIH-MGC <http://mgc.nhl.nih.gov/>  
National Institutes of Health  
Mammalian Gene Collection (MGC)  
AUTHORS  
TITLE

5. 2. 15

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM13573 row: d column: 24  
High quality sequence stop: 607.

## FEATURES

source

Location/Qualifiers  
1..931

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6184295"  
/clone\_lib="Lupski\_dorsal\_root\_ganglion"  
/sex="male"  
/tissue\_type="dorsal root ganglia"  
/dev\_stage="adult, 36 yr"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6 (Life Technologies); Site\_1:  
NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCACGAGTCCG-3' and  
5'-GACTGATCTTAGATGCGAGCGGCGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.7 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

BASE COUNT 218 a 283 c 224 g 204 t 2 others  
ORIGIN

## Alignment Scores:

Pred. No.: 2,35e-92 Length: 931  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conserved: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-09-882-735-2 (1-161) x BQ723672 (1-931)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
Db 11 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATGATTCCTGTAC 70  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40  
Db 71 AAGTGTCCCAAGAAAGAACTACTGTACAAATGACTGTCCAGGCCCGGGGCGAGATACG 130  
QY 41 CysArgGlnCysGlnSerSerPheThrValSerGlnAsnHisLeuArgHisCysLeu 60  
Db 111 TCGACGAGAGTGTGAAGGCGCTCTCCACCGCTTCAGAAACACCGCTCAGACACTG 190  
QY 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
Db 141 AATGTGTGTAATGTCCCAAGAAATATATCCACCTCAAAATATGATTCCTGTAC 250  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlnAsnLeu 100  
Db 241 CCGACACCGCTGT 310  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGln 120  
Db 311 TCGACGAGAGTGTGAAGGCGCTCTCCACCGCTTCAGAAACACCGCTCAGACACTG 370  
QY 121 LysThrAspThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140  
Db 371 AAAAGAGACCGGT 430

QY 141 SerCysSerAsnCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGln 160  
Db 421 TCGTGTAGTACTGTAGAAAGCGCTGAGATGTCAGACAAAGTGTGCTACCCAGATTGAG 490  
QY 161 Asn 161  
Db 491 AAT 493

## RESULT 2

AL559050 957 bp mRNA linear EST 16-FEB-2001

## LOCUS

AL559050 LIT\_NFL008\_TC2 Homo sapiens cDNA clone CS0DD010YB05 5

## DEFINITION

prime, mRNA sequence.

## ACCESSION

AL559050 GI:12904166

## VERSION

EST.

## KEYWORDS

SCURCE

## ORGANISM

human.

## REFERENCE

1. (bases 1 to 957)

## AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

## TITLE

Full-length cDNA libraries and normalization

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

## FEATURES

source

1..957

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DD010YB05"

/clone\_lib="LIT\_NFL008\_TC2"

/sex="male"

/tissue\_type="T cells from T cell leukemia"

/note="Vector: PCMVSPORT 6; Site\_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the PCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com"

BASE COUNT 222 a 262 c 252 g 220 t 1 others

## ORIGIN

1 others

## Alignment Scores:

Pred. No.: 2,45e-92 Length: 957  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conserved: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-882-735-2 (1-161) x AL559050 (1-957)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
Db 313 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATGATTCGTTGCTGTAC 372  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40  
Db 373 AAGTGTCCCAAGAAAGAACTACTGTACAAATGACTGTCCAGGCCCGGGGCGAGATAC 432  
QY 41 CysArgGlnCysGlnSerSerPheThrValSerGlnAsnHisLeuArgHisCysLeu 60  
Db 433 TCGACGAGAGTGTGAAGGCGCTCTCCACCGCTTCAGAAACACCGCTCAGACACTG 492  
QY 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80

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Db 493 ACTGCTGCAAAATGCGGAAATGCTGAGGTGAGATCTTTCTTCCACAGTGGAC 552
Oy 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTTPSerGluAsnLeu 100
Db 553 CAGGATACCTGCTGTTGATGAGAGAAAGAGTACAGGATATTATTGAGTGAAGACCTT 612
Oy 101 PheGlnCysPheAsnCysSerLysCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 613 TTCCAGTGTCTTCAATTCAGCTTCTGCTTAAATGAGAGCTGACCTCTCTCTCCAGAGAG 672
Oy 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db 673 AAAACAGAACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 732
Oy 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
Db 733 TCTGTAGTAACTGTAACAAAAGAGCTGATGATGATGATGATGATGATGATGATGATGAT 792
Oy 161 Asn 161
Db 793 AAT 795

RESULT 3
LOCUS RG180101 974 bp mRNA linear EST 06-FEB-2001
DEFINITION 602129676P1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',
mRNA sequence.
ACCESSION RG180101
VERSION RG180101.1 GI:125684804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10185, row: g, column: 20
High quality sequence stop 657
FEATURES
Location/Qualifiers
BASE COUNT 259 a 265 c 265 g 185 t
ORIGIN
1..974
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4431019"
/tissue_type="adrenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: Not I;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

```

```

us-09 882-735.2 (1 161) x RG180101 (1 974)
Oy 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20
Db 118 CATAGTGTGTGTCCTCCCAAGGAAATATATGCAAGTCACTTAAAAATATTGAAATTTTATG 177
Oy 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysPheGlyPheGlyGlnAspThrAsp 40
Db 178 AAGTCCACACAAAAGAACTACTTGTGTAATATATTTTAAAGAGGAGGAGGAGGAGGAGGAG 247
Oy 41 CysArgGluCysGluSerGlySerPheThrAlaSerSerAsnHisLeuArgHisCysLeu 60
Db 238 TCGAGGAGAGTGTGAGAGCTGCTTCTTACGCTTCTCAAAAAACACCTCAAGATATGATCT 297
Oy 61 SerCysSerLysCysAspGlyLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
Db 298 AGTGTCTTCTTAAATGCTTCAAAAGGAAATGAGTCAATGATGATGATGATGATGATGATG 347
Oy 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTTPSerGluAsnLeu 100
Db 358 CCGGACACCCGTGTGCTGCTGACGAGAACCACTATATTAAGTAAAAAGCTT 417
Oy 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnIleGlu 120
Db 418 TTCAGTGTCTTCAATTCAGCTTCTGCTTCAAGGAGAGAGTGAACCTGCTTCTTCTTCTT 477
Oy 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db 478 AAAACAGAACACCCGTGTGCTGCTGACCTGCTGATGATGATGATGATGATGATGATGATG 537
Oy 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
Db 538 TCTGTAGTAACTGTAAGAAAGAGCTGAGTGAAGAAATTTGCTATATGTAAGATTAAAT 597
Oy 161 Asn 161
Db 598 AAT 600

RESULT 4
LOCUS AU131978 761 bp mRNA linear EST 01-AUG-2002
DEFINITION AU131978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
sequence.
ACCESSION AU131978
VERSION AU131978.1 GI:10992132
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S., and
Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisakazu, Chiba 292 0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
BASE COUNT 259 a 265 c 265 g 185 t
ORIGIN
1..761
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP3003570"
/location="Chiba, Japan"

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/cell_type="teratocarcinoma"
/cell_line="NT2"
/notes="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 178 a 199 c 201 g 179 t 4 others
ORIGIN

```

## Alignment Scores:

Pred. No.	Length	Matches	Conservative	Mismatches	Indels	Gaps
937.00	761	160	0	1	0	0
Percent Similarity:	99.38%					
Best Local Similarity:	99.38%					
Query Match:	99.57%					

US-09-882-735-2 (1-161) x A0131978 (1-761)

```

QY 1 AspSerValCysProGlnGlyLysTyrLLeHisProGlnHisAsnSerIleCysCysThr 20
Db 182 GATACGTGTGTGTCCTCCAGGAAATATATCCACCTTCAAAATATTCGATTCTGTACC 241
QY 21 LysCysHisLysGlyThrTyrLeuCysAsnAspCysProGlyProGlyGlnAspThrAsp 40
Db 242 AAGTCCCAAGAGAACTACTGTGACATGATGTCACAGGCCCGGGGAGATACGGAC 301
QY 41 CysArgGluCysGluSerGlySerThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db 302 TCCAGGAGATGTGAGAGAGGAGGCTCTTCACCCCTTCAGAAAACCACTCAGACAGTGCCTC 361
QY 61 SerCysSerLysCysArgLysGlyLysMetGlyGlnValGlnLeuSerSerCysThrValAsp 80
Db 362 AGTTGTTTAAATGTCGAAAABAAATGAGTCAAGTGGAGATCTCTTTCGACACAGTGGAC 421
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
Db 422 CCGGACACCGGTGTGTGCTGACAGAGACAGTACCGGATTAATGAGATGAAAACCTT 481
QY 121 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 482 TTCCAGTGTCTTCAATGAGAGGCTCTGCTTCATATGAGACCGTGCCTCTCCACAGGAG 541
QY 141 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db 542 AAACGAGAACCGGTGTGTGACCTGCAATGAGATGTTCTTTCTAGAGAAAACGAGTGTGC 601
QY 161 SerCysSerAsnGlyLysLysSerLeuGluCysThrTyrLeuCysLeuProGlnIleGlu 160
Db 602 TACTATATTAACCTGTAAAGAAAACCTGAGTGTGAGAGAGTGTGCTTACCCAGATTGAG 661
QY 161 Asn 161
Db 662 AAT 664

```

RESULT 5  
AL522989 837 bp mRNA linear EST 13-FEB-2001  
LOCUS  
DEFINITION AL522989.1 IT1\_NFL004\_2802 Homo sapiens cDNA clone CG0DB009YPI4 5  
ACCESSION  
VERSION AL522989.1 GI:12786452  
KEYWORDS  
SOURCE  
ORGANISM human.  
Human sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 837)  
AUTHORS Li, W. B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr.

## FEATURES

source

Location/Qualifiers  
1..837

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DB009YPI4"  
/clone\_1ib="LTI\_NFL004\_NBC2"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 199 a 231 c 229 g 177 t 1 others  
ORIGIN

## Alignment Scores:

Pred. No.	Length	Matches	Conservative	Mismatches	Indels	Gaps
1.9e-91	837	160	0	1	0	0
Score:	932.00					
Percent Similarity:	99.38%					
Best Local Similarity:	99.38%					
Query Match:	99.04%					

US-09-882-735-2 (1-161) x AL522989 (1-837)

```

QY 1 AspSerValCysProGlnGlyLysTyrLLeHisProGlnHisAsnSerIleCysCysThr 20
Db 318 GATAGTGTGTGTCCTCCAGGAAATATATCCACCTTCAAAATTAATTCGATTGCTGTACC 377
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
Db 378 AAGTCCCAAGAGAACTACTGTGACATGATGTCACAGGCCCGGGGAGATACGGAC 437
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db 438 TGCAGGAGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTCAGACAGCTTC 497
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnLeuSerSerCysThrValAsp 80
Db 498 AGCTGCTCCAAAGCCGAAAGAAATGGGTGAGTGTGAGATCTCTTCTTGACAGTGGAC 557
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
Db 558 CGGACACCGTGTGTGCTGACAGAGAACCGATCCGCATTTATGGATGAAAACCTT 617
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 618 TTCAGTGTCTTCAATGACACCTCTGCTCAATGGAGACCGTGCACCTCTCTGACAGAG 677
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db 678 AAACGAGAACCGGTGTGTGACCTGCAATGAGATGTTCTTTCTAAGAGAAAACGAGTGTGC 737
QY 141 SerCysSerAsnGlyLysLysSerLeuGluCysThrTyrLeuCysLeuProGlnIleGlu 160
Db 738 TCCGTGATTAACCTGTAAAGAAAACCTGAGATGACCAATTTGTACTACCCAGATTGAG 797
QY 161 Asn 161
Db 798 AAT 800

```

RESULT 6  
BM546826 1070 bp mRNA linear EST 20-FEB-2002  
LOCUS  
DEFINITION BM546826 1070 bp mRNA linear EST 20-FEB-2002  
AGENCOURT 6491128 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5723557  
5', mRNA sequence.

```

ACCESSION   RM546826
VERSION     RM546826.1  GI:14780094
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1070)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12711 row: g column: 14
            High quality sequence start: 2
            High quality sequence stop: 669.
FEATURES    Location/Qualifiers
            source          1..1070
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                        /db_xref="taxon:9606"
                        /clone="IMAGE:5723557"
                        /clone_lib="NIH_MGC_125"
                        /lab_host="DH10B"
                        /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                        Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
                        of three ovaries, from females ranging in age from 38 to
                        49 yo. Library is oligo-dT primed and directionally cloned
                        (EcoRV site is destroyed upon cloning). Average insert
                        size 2.1 kb, insert size range 1-3.5 kb. Library is
                        normalized and enriched for full-length clones and was
                        constructed by C. Gruber (Invitrogen) Research Genetics
                        tracking code 036."
BASE COUNT   241 a 311 c 293 g 224 t 1 others
ORIGIN
Alignment Scores:
Pred. No.:    3,66e-91      Length:    1070
Score:        931.00      Matches:    159
Percent Similarity: 99.38%      Conservative: 1
Best Local Similarity: 98.76%      Mismatches: 1
Query Match: 98.94%      Indels: 0
DB:           13      Gaps: 0

US-09-882-735-2 (1-161) x RM546826 (1-1070)
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20
DB 326 GATATGCTGCTGCTCCCAAGGAAATATATATACACCTCAAAATAATTGCTGATCC 385
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40
DB 386 AAGTGTGCACAAAGGAACCTACTTGACAAATGACTGTCCAGGCGCGGAGATACGAC 445
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
DB 446 TTAGAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 505
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 506 ACTGTCTCAATATCGAAAGAAATGAGTTCAGGTGAGATCTCTTTTCACAGTGGAC 565
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 566 CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120

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DB 626 TTCAGTCTCTCAATTCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 140
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAspGlnCysVal 140
DB 686 AAAAGAAACACACGCTGTAATCTGCAATGTAAGTCTCTCTCTCTCTCTCTCTCTCT 145
QY 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 746 TCCGTGTAACTTAAAGAAAGGCTGTAATCTGCAATGTAAGTCTCTCTCTCTCTCT 160
QY 161 Asn 161
DB 806 AAT 808
RESULT 7
BM8000044
LOCUS       BM8000044
DEFINITION  BM8000044 6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5723557
            5', mRNA sequence.
ACCESSION   BM8000044
VERSION     BM8000044.1 GI:19116867
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 994)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12212 row: b column: 02
            High quality sequence stop: 654.
FEATURES    Location/Qualifiers
            source          1..994
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:5531041"
                        /clone_lib="NIH_MGC_71"
                        /tissue_type="leiomyosarcoma"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: uterus, Vector: pCMV-SPORT6, Site 1: NotI;
                        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 2.1 kb."
BASE COUNT   233 a 284 c 262 g 212 t
ORIGIN
Alignment Scores:
Pred. No.:    1.1e-89      Length:    994
Score:        917.00      Matches:    156
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.36%      Mismatches: 0
Query Match: 97.45%      Indels: 0
DB:           14      Gaps: 0

US-09-882-735-2 (1-161) x BM800044 (1-994)
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20
DB 286 GATATGCTGCTGCTCCCAAGGAAATATATATACACCTCAAAATAATTGCTGATCC 140
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40
DB 346 AAGTGTGCACAAAGGAACCTACTTGACAAATGACTGTCCAGGCGCGGAGATACGAC 405

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BASE COAT  
PRIMER

AUTHORS	TITLE	JOURNAL	COMMENT
L.W.B., Gruber,C., Jessee,J. and Polayes,D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seq@genoscope.cns.fr, web: www.genoscope.cns.fr
FEATURES	source		
	1..975		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="CSOD1082YA01"		
	/clone_lib="WT1.NFL006.PL2"		
	/tissue_type="placenta"		

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/note=vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT)_primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
```



[illegible]

Cy	140	SctgYsserXenCySylSyScrlcGlnCytThrLysLeuYsleuProGlnIleGl	160
Dh	774	CTTGGTGATGAATTAAAGATAACCGTTGAGTCAGCAAGA- TTGGACTTAAGCCCATGTGA	832
OY	160	UASHN 161     	
Db	833	GAAT 836	
<b>RESULT 12</b>			
	BES71809	969 bp	mRNA linear EST 20-Oct-2000
	Locus:	NH-MGC_65 Homo sapiens cDNA clone IMAGE:385255 5'	
	DEFINITION:	MMA sequence.	
	VERSION:	BES71809	
	KEYWORDS:	BES71809.1 GI:10320585	
	SOURCE:	EST.	
	ORGANISM:	human.	
	REFERENCE:	Homo sapiens	
AUTHORS:	Euryzota, Matarca; Chordata; Craniata; Vertebrata, Eutelestomi;		
TITLE:	Mammalia, Eutheria; Primates, Catarrhini; Homidae, Hemo-		
JOURNAL:	NIH-MGC http://mgs.nci.nih.gov/ (bases 1 to 969)		
COMMENT:	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM974 row: 0 column: 22 High quality sequence stop: 642.		
FEATURES	Location/Qualifiers		
source	1..969	/organism="Homo sapiens"	
	/db_xref="taxon:9606"		
	/clone="IMAGE:385255"		
	/clone_id="NIH_MGC_65"		
	/tissue_type="adenocarcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: colon; Vector: PCMV-SPORT6, Site: 1, Notif: site_2; Salt: cloned unidirectionally. PrimerT_Oligo dt. Average insert size 1.8 kc. Library constructed by Life Technologies."		
BASE COUNT	281 a 273 c 241 g 174 t		
ORIGIN	"		
Alignment Scores:			
Pred. No.: 1.52e-85	length: 969		
Score: 879.00	Matches: 153		
Percent Similarity: 98.71%	Conservative: 0		
Best Local Similarity: 98.71%	Mismatches: 1		
Query Match: 93.41%	Indels: 1		
DB: 12	Gaps: 0		
US-09-882-735-2 (1-161) x BES71809 (1-969)			
OY	8	LysTYrIlentIs-ProGInAsnAnSerIleCYsCYeThrLYsCYshISlySGlThRTY	27
Db	2	AAATATATCCCGCGCTCAAAATATATTCATTGCCGTGACCAGIGCCACAAGSAACCTA	61
CY	27	rLeuTYrAsnaSPcySProGIyPROGLyGInASPTThrASPcyArGclucySGIUserGI	47
Db	62	CTTAGCACATACAGTGTCTAGSCGCGGAGGAGATAGGAGCTGAGGAGGTGAGAGCGG	121
CY	47	ySerPheThrAlaserguASnhISleAuGHISCYseuSeuerysSerlysCYsarGly	67
Db	122	CTCCCTACCGGCTTAGAAAACCACTGAGCACTGCTCCTGAGCTCCCAAATGCCAAA	181





/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/note "Vector: pEX18SFT3; mRNA from undifferentiated precursor cells"  
BASE COUNT 204 a 261 c 243 g 208 t 3 others  
ORIGIN

## Alignment Scores:

Alignment Scores:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Pred. No.:	5,38-84	845	154	2	2	0
Score:	864.00					
Percent Similarity:	97.60%					
Best Local Similarity:	96.08%					
Query Match:	91.90%					

US-09-882-735-2 (1-161) x NIH57305 (1-845)

OR 1 Aspergillus fumigatus proteinase B (PF00089) [Fungi] 20  
26 340 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCAAAATTCGATTGCTGTAAC 359  
OR 21 LysCysHisLysGlyThrThrLeuTyrAspCysProGlyProGlyGlnAspThrAsp 40  
26 470 AAGTGTGAAAGAAAGAAAT 459  
OR 41 CysAspThrValCysGlyCysArgLysSerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
26 460 TGGAGGAG 519  
OR 41 SerCysSerLysCysArgLysMetGlyValGlnLeuSerSerCysThrValAsp 80  
26 520 AAGTGTGAAAGAAAGAAAT 579  
OR 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
26 560 GAGGAG 639  
OR 101 PheGlnCysPheAsnGlySerLeuGlySerLeuAsnGlyThrValHisLeuSerCysGlnGln 120  
26 640 TTTCCGCTCTTCAATTCGAGGAG 699  
OR 101 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlnCysVal 140  
26 740 AAGGAG 758  
OR 141 SerCysSerLysCysArgLysSerLeuGlnCysThrHisLeuSerCysLeuProGlnLeu 160  
26 789 TTTCTGTACTAAGTGAAGAAAG 817  
RESULT 15  
LOCUS B1757305 916 bp mRNA linear EST 25-SEP-2001  
DEFINITION Homo sapiens cDNA clone IMAGE519749 5',  
mRNA sequence.  
ACCESSION B1757305  
VERSION B1757305.1 GI:15748883  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.  
REFERENCE 1 (bases 1 to 916)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Straussberg, Ph.D.  
Email: gsgaps-f@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I M A G E Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LIAK1500 row: f column: 06  
High quality sequence stp. 827.  
Location/Qualifiers  
1. 916  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:519749"  
/clone\_id="NIH\_MGC\_114"  
/lab\_host="DH10B"  
/note="Organ. Brain; Vector: pCMV-SPORT6; Site 1. Not a  
male brains age range 23-27 yr. Library is 0.15-0.8T  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH MGC library."

## FEATURES

source

BASE COUNT 204 a 261 c 243 g 208 t  
ORIGIN

## Alignment Scores:

Alignment Scores:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Pred. No.:	1,886-83	916	153	2	3	1
Score:	859.50					
Percent Similarity:	96.27%					
Best Local Similarity:	95.03%					
Query Match:	91.34%					

US-09-882-735-2 (1-161) x B1757305 (1-916)

OR 1 Aspergillus fumigatus proteinase B (PF00089) [Fungi] 20  
26 291 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCAAAATTCGATTGCTGTAAC 350  
OR 21 LysCysHisLysGlyThrThrLeuTyrAspCysProGlyProGlyGlnAspThrAsp 40  
26 351 AAGTGTGAAAGAAAGAAAT 410  
OR 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
26 411 TCCAGGAG 470  
OR 61 SerCysSerLysCysArgLysGlnMetGlyValGlnLeuSerSerCysThrValAsp 80  
26 471 AGCTGCTCCAAATGCGAAGAGAAATGGGTCAGAGTGAATCTTCTTTCGACAGTGGAC 530  
OR 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
26 531 CGGAGACACCGGTGTGGCTGCAGAGAAACAGTACCGGCATATATGAGAGAAACCT 590  
OR 100 PheGlnCysPheAsnGlySerLeuGlySerLeuAsnGlyThrValHisLeuSerCysGln 120  
26 591 TTTCCGCTCTTCAATTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650  
OR 120 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlnCysVal 140  
26 651 AAGGAG 710  
OR 140 AlSerCysSerLysCysArgLysSerLeuGlnCysThrHisLeuSerCysLeuProGln 158  
26 711 TTTCTGTACTAAGTGAAGAAAG 769

Search completed: January 6, 2003, 06:44:26  
Job time: 2219 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

QM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 01:14:03 ; Search time 2774 Seconds  
(without alignments)  
5067 287 Million cell updates/sec

Title: US-09-882-735-1  
Perfect score: 483  
Sequence: 1 gaaatgtgtgtcccaagg ... gactaccacagattgagaat 483

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 1455140287A residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.in.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.mu.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	483	100.0	483	6	A29099	A29099 Synthet
2	483	100.0	483	6	AP174442	AP174442 Sequen
3	483	100.0	1301	6	AR111310	AR111310 Sequen
4	483	100.0	1301	6	AR134762	AR134762 Sequen
5	483	100.0	1331	6	A29103	A29103 H.sapien
6	483	100.0	1368	6	A29098	A29098 Synthet
7	483	100.0	2050	9	HUMTNFRP	M60275 Human Tumor
8	483	100.0	2062	6	A21522	A21522 TNF alpha
9	483	100.0	2062	6	I43805	I43805 Sequence
10	483	100.0	2067	9	HUMTNFR	M43794 Human Tumor
11	483	100.0	2159	9	AK956611	AK956611 Homo sapi
12	483	100.0	2111	6	A26412	A26412 cDNA for
13	483	100.0	2111	6	AX409713	AX409713 Sequence
14	483	100.0	2111	9	HUMTNFRB	M59286 Homo sapien
15	483	100.0	2112	9	HUMTNFRC	M64121 Human Tumor
16	483	100.0	2161	6	AP096330	AP096330 Sequence
17	483	100.0	2161	9	HSTNFR1A	X55113 H.sapien
18	483	100.0	2175	6	A43873	A43873 Sequence
19	483	100.0	2175	6	A78738	A78738 Sequence
20	483	100.0	2175	6	AR041076	AR041076 Sequence
21	483	100.0	2175	6	I64751	I64751 Sequence
22	483	100.0	2176	6	AI9907	AI9907 Synthet
23	483	100.0	2194	9	BC010140	BC010140 Homo sapi
24	483	100.0	6889	6	I26928	I26928 Sequence
25	483	100.0	6896	6	AR031375	AR031375 Sequence
26	483	100.0	6896	6	BD009743	BD009743 Compos
27	478.4	99.0	600	6	A29257	A29257 Synthet
28	477	98.8	510	6	A21525	A21525 ol.venue
29	475.2	98.4	600	6	I43808	I43808 Sequence
30	475	98.3	1147	6	AR131309	AR131309 Sequence
31	475	98.3	1147	6	AR134761	AR134761 Sequen
32	471	97.5	2061	6	A29255	A29255 cDNA for
33	424.4	87.9	1049	6	AR131307	AR131307 Sequen
34	424.4	87.9	1049	6	AR134759	AR134759 Sequen
35	424.4	87.9	1202	6	AR131308	AR131308 Sequen
36	424.4	87.9	1202	6	AR134760	AR134760 Sequen
37	383	79.3	504	6	A20713	A20713 Synthet
38	383	79.3	504	6	I43813	I43813 Sequence
39	381	78.9	501	6	I43786	I43786 Sequence
40	379.8	78.6	1977	6	AX404869	AX404869 Sequen
41	372	77.0	372	6	A20253	A20253 Synthet
42	372	77.0	372	6	I43787	I43787 Sequence
43	369	76.4	500	6	A20254	A20254 Synthet
44	358.2	74.2	2171	4	AB051103	AB051103 Fetus
45	357.2	74.0	474	6	A29259	A29259 Synthet

ALIGNMENTS

RESULT 1  
A29099  
LOCUS A29099 483 bp DNA linear PAT 03 JUL 1996  
DEFINITION Synthetic DNA for TNF-binding polypeptide from patent EP040408.  
ACCESSION A29099  
VERSION A29099.1 GI:1248893  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 483)  
AUTHORS Hauptmann,R., Himmler,A., Maurer-Fogy,I. and Stratowa,T.  
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
JOURNAL Patent: Ep 0194438 A 49 24-OCT-1990;  
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H.

